



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 106612**

**To: Sumesh Kaushal**  
**Location: CM1/12A07/11E12**  
**Art Unit: 1636**  
**Tuesday, October 28, 2003**

**Case Serial Number: 09/925674**

**From: Beverly Shears**  
**Location: Biotech-Chem Library**  
**CM1-1E05**  
**Phone: 308-4994**

**beverly.shears@uspto.gov**

### **Search Notes**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:27:45 ; Search time 60 Seconds  
(without alignments)  
510.570 Million cell updates/sec

Title: US-09-925-674A-7  
Perfect score: 1007  
Sequence: 1 MATPASAPCTRALVADFVG.....LTGAVALGALVTVGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A Geneseq 19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
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7: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:\*  
9: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:\*  
10: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:\*  
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12: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:\*  
13: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:\*  
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15: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:\*  
16: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:\*  
17: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:\*  
18: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1007	100.0	193	20 AAY05530	Human Bcl-w protei
2	1002	99.5	193	19 AAW61392	Human bcl-y protei
3	1002	99.5	193	20 AAW97392	The human bcl-y pr
4	1000	99.3	193	18 AAW36047	Human bcl-w protei
5	1000	99.3	193	20 AAY05531	Mouse Bcl-w protei
6	1000	99.3	193	20 AAY05532	Human Bcl-w protei
7	997	99.0	192	20 AAW97394	Mammalian bcl-y pr
8	996	98.9	193	19 AAW61391	Rat bcl-y protein.
9	996	98.9	193	20 AAW97391	The rat bcl-y prot

10	991	98.4	192	20 AAW97393	Protein sequence o
11	958.5	95.2	192	20 AAY05533	Mouse Bcl-w protei
12	867	86.1	168	18 AAW36048	Mouse bcl-w protei
13	821.5	81.6	190	23 AAO18223	Human Bcl-Rambo BH
14	766	76.1	365	19 AAW59884	Amino acid sequenc
15	766	76.1	365	23 ABG95556	Human novel secret
16	433.5	43.0	411	22 AAU00219	Bcl-Xl-DTR apoptos
17	431.5	42.9	237	23 ABG78480	wild type BclXl pr
18	428.5	42.6	233	16 AAR68887	Human thymus BCL-X
19	428.5	42.6	233	17 AAW05821	Bcl-XL protein. H
20	428.5	42.6	233	18 AAW31530	Human anti-apoptot
21	428.5	42.6	233	21 AAY81323	Bcl-x polypeptide.
22	428.5	42.6	233	21 AAY69969	Human Bcl-XL prote
23	428.5	42.6	233	22 AAG64262	Human Bcl-XL prote
24	428.5	42.6	233	22 AAB73303	Rat wild-type Bcl-
25	428.5	42.6	233	22 AAB50538	Human Bcl-XL prote
26	428.5	42.6	233	22 AAB47515	Protein encoded by
27	425	42.2	225	18 AAW19396	"Deprenyl" (RTM)-i
28	424.5	42.2	233	22 AAB73304	Mutant rat Bcl-XL
29	416.5	41.4	239	22 AAG64037	Human Bcl-2 protei
30	415.5	41.3	152	24 AAG79760	Bcl-XL. Homo sap:
31	413	41.0	236	22 AAB35131	Murine Bcl-2. Mus
32	413	41.0	236	23 AAU76554	Murine Bcl-2 polyp
33	412.5	41.0	239	20 AAW87810	A human Bcl-2 prot
34	412.5	41.0	239	22 AAB74127	Human bcl-2. Homo
35	412.5	41.0	239	22 AAB35130	Human Bcl-2. Homo
36	412.5	41.0	239	23 ABG78478	Human Bcl2 mutant
37	412.5	41.0	239	23 ABG78479	Human Bcl2 mutant
38	412.5	41.0	239	23 AAU76553	Human Bcl-2 polype
39	412.5	41.0	272	24 ABR41675	Human DITHP cel m
40	410.5	40.8	239	9 AAP80987	Sequence of bcl-2-
41	410.5	40.8	239	14 AAR42312	Bcl-2 oncogene pro
42	410.5	40.8	239	16 AAR70331	Human bcl-2 protei
43	410.5	40.8	239	16 AAR71404	Human bcl-2 alpha
44	410.5	40.8	239	19 AAW40217	Human bcl-2. Homo
45	410.5	40.8	239	20 AAW87812	A human Bcl-2-alph

ALIGNMENTS

RESULT 1  
AAY05530  
ID AAY05530 standard; Protein; 193 AA.  
XX  
AC AAY05530;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human Bcl-w protein essential for spermatogenesis.  
XX  
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
KW animal model.  
XX  
OS Homo sapiens.  
XX  
PN WO9913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU00764.  
XX  
PR 16-SEP-1997; 97AU-0009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
XX  
DR WPI; 1999-243890/20.  
DR N-PSDB; AAX25132.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w

XX Claim 2; Page 33; 52pp; English.

PS The present sequence is human Bcl-w, a pro-survival member of the

XX Bcl-2 family which is widely expressed and which is essential for

CC spermatogenesis. The invention relates generally to a method of

CC treatment and to an animal model for the identification of

CC molecules and genetic sequences useful for inducing or reducing

CC fertility of male animals. Methods are provided for the treatment

CC of infertility, or for reducing fertility, by modulating

CC spermatogenesis. An animal model carries a mutation is at least

CC one allele of the human or murine bcl-w gene (see AAX25132-35) or in

CC a gene associated with bcl-w. Such animals have disorganised

CC seminiferous tubules and are substantially infertile, but possess no

CC other major abnormalities as determined by histological examination.

CC They can be used to screen for therapeutic molecules including

CC genetic sequences capable of inducing, enhancing or otherwise

CC facilitating spermatogenesis in animals, or which can induce

CC infertility.

XX Sequence 193 AA;

SQ

Query Match 100.0%; Score 1007; DB 20; Length 193;

Best Local Similarity 100.0%; Pred. No. 3.4e-103;

Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

DB 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

QY 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVG 120

DB 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVG 120

QY 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARRLREGNWSVRTVLTGAVAL 180

DB 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARRLREGNWSVRTVLTGAVAL 180

QY 181 GALVTVGGAFFASK 193

DB 181 GALVTVGGAFFASK 193

RESULT 2

AAW61392

ID AAW61392 standard; Protein; 193 AA.

XX AAW61392;

AC

XX 02-OCT-1998 (first entry;

DE Human bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.

XX Homo sapiens.

OS US5789201-A.

PN 04-AUG-1998.

PD 11-FEB-1997; 97US-0798897.

PF 23-FEB-1996; 96US-0012201.

PR 11-FEB-1997; 97US-0798897.

XX (COCE-) COCENSYS INC.

PA Guasteilla J;

PI WPI; 1998-446079/38.

XX N-PSDB; AAV28334.

PT Nucleic acids encoding B-cell lymphoma-y protein - useful for

PT producing recombinant protein for use in treating uncontrolled cell

PT growth e.g. cancers

XX Example; Column 17/18; 27pp; English.

PS The mammalian bcl-y protein is a member of the bcl-2 family, components

XX in the cell death pathway. The bcl-2 family have both apoptotic activity

CC and the apoptosis blocking activity. bcl-y falls in the apoptosis

CC activity category. The recombinant protein may be used to prevent

CC uncontrolled cell growth, either by its direct administration to

CC recombinant genetic constructs to increase its expression in vivo. Also,

CC antisense constructs can be used in disorders where prevention of cell

CC death is desired.

XX Sequence 193 AA;

SQ

Query Match 99.5%; Score 1002; DB 19; Length 193;

Best Local Similarity 99.5%; Pred. No. 1.2e-102;

Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

DB 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60

QY 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVG 120

DB 61 FSDLAALQHLVTPGSAQQRFTQVSDDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVG 120

QY 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARRLREGNWSVRTVLTGAVAL 180

DB 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGCALEEARRLREGNWSVRTVLTGAVAL 180

QY 181 GALVTVGGAFFASK 193

DB 181 GALVTVGGAFFASK 193

RESULT 3

AAW97392

ID AAW97392 standard; Protein; 193 AA.

XX AAW97392;

AC

XX 20-MAY-1999 (first entry)

DE The human bcl-y protein.

XX Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;

KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;

KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;

KW multiple sclerosis; myocardial infarction; vitally induced cell death;

KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;

KW premature cell death; cell death stimulator; prolonged cell life span;

KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;

KW parasite.

XX Homo sapiens.

OS US5883229-A.

PN 16-MAR-1999.

PD 25-NOV-1997; 97US-0978523.

PF 23-FEB-1996; 96US-0012201.

PR 11-FEB-1997; 97US-0798897.

PR 25-NOV-1997; 97US-0978523.

XX (COCE-) COCENSYS INC.

PA Guastella J;

PI

XX

DR WPI; 1999-214150/18.  
DR N-PSDB; AAX15946.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
for modulating programmed cell death  
XX  
PS Claim 1; Columns 17-18; 26pp; English.  
XX  
CC The present sequence represents human bcl-y protein (Hbcl-y). The  
specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and  
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral  
CC sclerosis- conditions where cells under go premature cell death as a  
CC result of triggers which may or may not be apparent. They may also be  
CC used in this way to develop cell lines which remain viable in culture for  
CC an extended period. In contrast, if they act as cell death stimulators,  
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with  
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and  
CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites.  
XX  
SQ Sequence 193 AA;  
Query Match 99.5%; Score 1002; DB 20; Length 193;  
Best Local Similarity 99.5%; Pred. No. 1.2e-102;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFGYKLRQKGVYCGAGPGEGPAADPLHOAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVEDFGYKLRQKGVYCGAGPGEGPAADPLHOAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHVTGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQLHVTGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWNASVRTVLTGAVAL 180  
DB 121 QVQEMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWNASVRTVLTGAVAL 180  
QY 181 GALVTVGGAFFASK 193  
b 181 GALVTVGGAFFASK 193  
RESULT 4  
AAW36047  
D AAW36047 standard; Protein; 193 AA.  
X  
C AAW36047;  
X  
T 22-APR-1998 (first entry)  
X  
E Human bcl-w protein.  
X Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
W diagnosis; degenerative disease.  
X  
S Homo sapiens.  
X  
N WO9735971-A1.  
X  
D 02-OCT-1997.  
X  
F 27-MAR-1997; 97WO-AU00199.  
X  
R 27-MAR-1996; 96AU-0008965.  
X

PA (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX  
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;  
XX  
DR WPI; 1997-489635/45.  
DR N-PSDB; AAT96577.  
XX  
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
or inhibit cell survival, e.g. for treatment of cancer and  
PT degenerative diseases  
XX  
PS Claim 6; Page 48; 86pp; English.  
XX  
CC This sequence represents a novel human protein, bcl-w, encoded by the  
bcl-2 gene family and extracted from an adult brain library. This gene  
CC promotes cell survival, so its modulation is useful in treatment of  
CC cancer or auto-immune diseases, degenerative diseases (e.g. stroke,  
CC Alzheimer's disease, myocardial infarct, muscular degeneration, hypoxia,  
CC ischaemia, human immunodeficiency virus infection or in cell transplants.  
CC Up-regulation of the gene can also be used to modify cell lines cultured  
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
CC and to increase survival of primary explants during genetic modification.  
CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
CC antibody production or screening of potential modulators.  
XX  
SQ Sequence 193 AA;  
Query Match 99.3%; Score 1000; DB 18; Length 193;  
Best Local Similarity 99.0%; Pred. No. 2e-102;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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DB 1 MATPASAPDTRALVADFGYKLRQKGVYCGAGPGEGPAADPLHOAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHVTGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQLHVTGSAQQRFTQVSDLEFGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWNASVRTVLTGAVAL 180  
DB 121 QVQEMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWNASVRTVLTGAVAL 180  
QY 181 GALVTVGGAFFASK 193  
DB 181 GALVTVGGAFFASK 193  
RESULT 5  
AAW05531  
ID AAW05531 standard; Protein; 193 AA.  
XX  
C AAW05531;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Mouse Bcl-w protein essential for spermatogenesis.  
X  
X Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
KW animal model.  
X  
OS Mus sp.  
XX  
PN WO9913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU00764.  
XX  
PR 16-SEP-1997; 97AU-0009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX



PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
XX WPI; 1999-243890/20.  
DR N-PSDB; AAX25133.  
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w  
XX Claim 2; Page 35; 52pp; English.  
PS The present sequence is mouse Bcl-w, a pro-survival member of the  
XX Bcl-2 family which is widely expressed and which is essential for  
CC spermatogenesis. The invention relates generally to a method of  
CC treatment and to an animal model for the identification of  
CC molecules and genetic sequences useful for inducing or reducing  
CC fertility of male animals. Methods are provided for the treatment  
CC of infertility, or for reducing fertility, by modulating  
CC spermatogenesis. An animal model carries a mutation is at least  
CC one allele of the human or murine bcl-w gene (see AAX25132-35) or in  
CC a gene associated with bcl-w. Such animals have disorganised  
CC seminiferous tubules and are substantially infertile, but possess no  
CC other major abnormalities as determined by histological examination.  
CC They can be used to screen for therapeutic molecules including  
CC genetic sequences capable of inducing, enhancing or otherwise  
CC facilitating spermatogenesis in animals, or which can induce  
CC infertility.  
XX Sequence 193 AA;  
SQ Query Match 99.3%; Score 1000; DB 20; Length 193;  
Best Local Similarity 99.0%; Pred. No. 2e-102;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASPTDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAAQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
DB 121 QVQDMMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
QY 181 GALVTVGGAFFASK 193  
DB 181 GALVTVGGAFFASK 193  
RESULT 6  
AAY05532  
ID AAY05532 standard; Protein; 193 AA.  
XX AAY05532;  
XX 05-JUL-1999 (first entry)  
DT Human Bcl-w protein essential for spermatogenesis.  
DE Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
XX animal model.  
KW Homo sapiens.  
XX WO9913710-A1.  
XX 25-MAR-1999.  
PD 16-SEP-1998; 98WO-AU00764.  
XX 16-SEP-1997; 97AU-0009228.  
PR 16-SEP-1997; 97AU-0009228.  
XX

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;  
XX WPI; 1999-243890/20.  
DR N-PSDB; AAX25134.  
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w  
XX Disclosure; Page 37; 52pp; English.  
PS The present sequence is described of a derivative of human Bcl-w  
XX (see also AAY05530), a pro-survival member of the Bcl-2 family that  
CC is widely expressed and which is essential for spermatogenesis.  
CC The invention relates generally to a method of treatment and to an  
CC animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male animals.  
CC Methods are provided for the treatment of infertility, or for  
CC reducing fertility, by modulating spermatogenesis. An animal model  
CC carries a mutation is at least one allele of the human or murine  
CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
CC Such animals have disorganised seminiferous tubules and are  
CC substantially infertile, but possess no other major abnormalities  
CC as determined by histological examination. They can be used to  
CC screen for therapeutic molecules including genetic sequences  
CC capable of inducing, enhancing or otherwise facilitating  
CC spermatogenesis in animals, or which can induce infertility.  
XX Sequence 193 AA;  
SQ Query Match 99.3%; Score 1000; DB 20; Length 193;  
Best Local Similarity 99.0%; Pred. No. 2e-102;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAAQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
DB 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLREGNWSVRTVLTGAVAL 180  
QY 181 GALVTVGGAFFASK 193  
DB 181 GALVTVGGAFFASK 193  
RESULT 7  
AAW97394  
ID AAW97394 standard; Protein; 192 AA.  
XX AAW97394;  
XX 20-MAY-1999 (first entry)  
DT Mammalian bcl-y protein.  
DE Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
XX programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
XX parasite.  
XX Mammalia.  
CS Mammalia.  
XX

PN US5883229-A.  
XX 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-0978523.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
PR 25-NOV-1997; 97US-0978523.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1999-214150/18.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
PT for modulating programmed cell death  
XX  
PS Claim 2; Columns 19-22; 26pp; English.  
XX  
CC The present sequence represents a mammalian bcl-1 protein.  
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein.  
CC thought to be involved in programmed cell death (apoptosis and necrosis).  
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
CC with a disruption of the cell death pathway. If they act as cell death  
CC inhibitors, they may be used in therapies to treat subjects suffering  
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
CC degenerative diseases (especially multiple sclerosis), myocardial  
CC infarction, vitally induced cell death, aging, spinal cord injuries and  
CC amyotrophic lateral sclerosis- conditions where cells under go premature  
CC cell death as a result of triggers which may or may not be apparent.  
CC They may also be used in this way to develop cell lines which remain  
CC viable in culture for an extended period. In contrast, if they act as  
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat  
CC conditions associated with prolonged cell life span such as cancer  
CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune  
CC diseases. They may also be used to cause cell death in, and hence  
CC control, parasites.  
XX  
SQ Sequence 192 AA;  
  
Query Match 99.0%; Score 997; DB 20; Length 192;  
Best Local Similarity 99.5%; Pred. No. 4.3e-102;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
QY 2 ATPASAPDTRALVADFVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 61  
DB 1 ATPASAPDTRALVEDFVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 60  
  
QY 62 SDLAAQLHVTTPGSAQQRFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVGQ 121  
DB 61 SDLAAQLHVTTPGSAQQRFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVGQ 120  
  
QY 122 VQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRREGNWASVRTVLTGAVALG 181  
DB 121 VQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRREGNWASVRTVLTGAVALG 180  
  
QY 182 ALVTVGAFPAASK 193  
DB 181 ALVTVGAFPAASK 192  
  
RESULT 8  
AAW61391  
ID AAW61391 standard; Protein; 193 AA.  
XX  
AC AAW61391;  
CX  
XT 02-OCT-1998 (first entry)  
CX  
XE Rat bcl-y protein.

XX bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
XX  
OS Rattus sp.  
XX  
PN US5789201-A.  
XX  
PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-0798897.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1998-446079/38.  
DR N-PSDB; AAV28333.  
XX  
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for  
PT producing recombinant protein for use in treating uncontrolled cell  
XX growth e.g. cancers  
PS Example; Fig 3A; 27pp; English.  
XX  
CC The mammalian bcl-y protein is a member of the bcl-2 family, components  
CC in the cell death pathway. The bcl-2 family have both apoptotic activity  
CC and the apoptosis blocking activity. bcl-y falls in the apoptosis  
CC activity category. The recombinant protein may be used to prevent  
CC uncontrolled cell growth, either by its direct administration to  
CC recombinant genetic constructs to increase its expression in vivo. Also,  
CC antisense constructs can be used in disorders where prevention of cell  
CC death is desired.  
XX  
SQ Sequence 193 AA;  
  
Query Match 98.9%; Score 996; DB 19; Length 193;  
Best Local Similarity 98.4%; Pred. No. 5.6e-102;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAAQLHVTTPGSAQQRFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
  
QY 121 VQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRREGNWASVRTVLTGAVAL 180  
DB 121 VQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRREGNWASVRTVLTGAVAL 180  
  
QY 181 GALVTVGAFPAASK 193  
DB 181 GALVTVGAFPAASK 193  
  
RESULT 9  
AAW97391  
ID AAW97391 standard; Protein; 193 AA.  
XX  
AC AAW97391;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE The rat bcl-y protein.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;

KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite.  
XX  
OS Rattus sp.  
XX  
PN US5883229-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-0978523.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
PR 25-NOV-1997; 97US-0978523.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1999-214150/18.  
DR N-PSDB; AAX15945.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
PT for modulating programmed cell death  
XX  
PS Disclosure; Columns 15-18; 26pp; English.  
XX  
CC The present sequence represents rat bcl-y protein (Rbcl-y). The  
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral  
CC sclerosis- conditions where cells under go premature cell death as a  
CC result of triggers which may or may not be apparent. They may also be  
CC used in this way to develop cell lines which remain viable in culture for  
CC an extended period. In contrast, if they act as cell death stimulators,  
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with  
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and  
CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites.  
XX  
SQ Sequence 193 AA;  
Query Match 98.9%; Score 996; DB 20; Length 193;  
Best Local Similarity 98.4%; Pred. No. 5.6e-102;  
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASTPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHVTTPGSAQQRFTQVSDelfQGGPNWGRVAFVFFVGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAALQLHVTTPGSAQQRFTQVSDelfQGGPNWGRVAFVFFVGAALCAESVNKEMEPLVG 120  
QY 121 QVQEWNVAYLETRLDWVHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180  
Db 121 QVQDWMVTYLETRLDWVHSSGGWAEFTALYGDGALEEARRLREGNWASVRTVLTGAVAL 180  
QY 181 GALVTVGAFVASK 193  
Db 181 GALVTVGAFVASK 193

RESULT 10  
AAW97393

ID AAW97393 standard; Protein; 192 AA.  
XX  
AC AAW97393;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE Protein sequence of the specification.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite.  
XX  
OS Unidentified.  
XX  
PN US5883229-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-0978523.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
PR 25-NOV-1997; 97US-0978523.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1999-214150/18.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
PT for modulating programmed cell death  
XX  
PS Disclosure; Columns 19-20; 26pp; English.  
XX  
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
CC thought to be involved in programmed cell death (apoptosis and necrosis).  
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
CC with a disruption of the cell death pathway. If they act as cell death  
CC inhibitors, they may be used in therapies to treat subjects suffering  
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
CC degenerative diseases (especially multiple sclerosis), myocardial  
CC infarction, vitally induced cell death, aging, spinal cord injuries and  
CC amyotrophic lateral sclerosis- conditions where cells under go premature  
CC cell death as a result of triggers which may or may not be apparent.  
CC They may also be used in this way to develop cell lines which remain  
CC viable in culture for an extended period. In contrast, if they act as  
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat  
CC conditions associated with prolonged cell life span such as cancer  
CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune  
CC diseases. They may also be used to cause cell death in, and hence  
CC control, parasites.  
XX  
SQ Sequence 192 AA;  
Query Match 98.4%; Score 991; DB 20; Length 192;  
Best Local Similarity 98.4%; Pred. No. 2e-101;  
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61  
Db 1 ATPASTPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAALQLHVTTPGSAQQRFTQVSDelfQGGPNWGRVAFVFFVGAALCAESVNKEMEPLVGQ 121  
Db 61 SDLAALQLHVTTPGSAQQRFTQVSDelfQGGPNWGRVAFVFFVGAALCAESVNKEMEPLVGQ 120

QY 122 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEAEARRLRREGNWSVRTVLTGAVALG 181  
Db 121 VQDWMVTYLETRLADWIHSSGGWAEFTALYGDGALEAEARRLRREGNWSVRTVLTGAVALG 180  
QY 182 ALVTVGGAFFASK 193  
Db 181 ALVTVGGAFFASK 192

RESULT 11  
AAAY05533  
ID AAY05533 standard; Protein; 192 AA.  
XX AC AAY05533;  
XX 05-JUL-1999 (first entry)  
XX Mouse Bcl-w protein deritvative.  
DE Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
KW animal model.  
XX OS Mus sp.  
XX WO9913710-A1.  
PN 25-MAR-1999.  
XX 16-SEP-1998; 98WO-AU00764.  
XX 16-SEP-1997; 97AU-0009228.  
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX PA Adams J, Cory S, Gibson L, Koentgen F, Print C;  
PI WPI; 1999-243890/20.  
XX N-PSDB; AAX25135.  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w  
XX Disclosure; Page 39; 52pp; English.

XX The present sequence is described of a derivative of mouse Bcl-w  
CC (see also AAY05531), a pro-survival member of the Bcl-2 family that  
CC is widely expressed and which is essential for spermatogenesis.  
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.  
CC The invention relates generally to a method of treatment and to an  
CC animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male animals.  
CC Methods are provided for the treatment of infertility, or for  
CC reducing fertility, by modulating spermatogenesis. An animal model  
CC carries a mutation is at least one allele of the human or murine  
CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
CC Such animals have disorganised seminiferous tubules and are  
CC substantially infertile, but possess no other major abnormalities  
CC as determined by histological examination. They can be used to  
CC screen for therapeutic molecules including genetic sequences  
CC capable of inducing, enhancing or otherwise facilitating  
CC spermatogenesis in animals, or which can induce infertility.

XX SQ Sequence 192 AA;  
Query Match 95.2%; Score 958.5; DB 20; Length 192;  
Best Local Similarity 94.8%; Pred. No. 7.9e-98;  
Matches 183; Conservative 6; Mismatches 3; Indels 1; Gaps 1;  
QY 1 MATPASAPDTRALVADFVGYKLQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTPGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120

Db 61 FSDLAAQLHVTPGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEAEARRLRREGNWSVRTVLTGAVAL 180  
Db 121 QVQDMIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRLRREGNWA-VSTVVTGAVAL 179  
QY 181 GALVTVGGAFFASK 193  
Db 180 GALVTVGGAFFASK 192

RESULT 12  
AAW36048  
ID AAW36048 standard; Protein; 168 AA.  
XX AC AAW36048;  
XX 22-APR-1998 (first entry)  
XX Mouse bcl-w protein.  
DE Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
XX diagnosis; degenerative disease.  
OS Mus sp.  
XX WO9735971-A1.  
XX 02-OCT-1997.  
XX 27-MAR-1997; 97WO-AU00199.  
XX 27-MAR-1996; 96AU-0008965.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
PI Adams JM, Cory S, Gibson LM, Holmgreen SP;  
XX WPI; 1997-489635/45.  
DR N-PSDB; AAT96578.

XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
PT or inhibit cell survival, e.g. for treatment of cancer and  
PT degenerative diseases  
XX Claim 6; Page 50-51; 86pp; English.  
XX This sequence represents a novel protein, bcl-w, encoded by the mouse  
CC bcl-2 gene family. This gene promotes cell survival, so its modulation  
CC is useful in treatment of cancer or auto-immune diseases, degenerative  
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular  
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection  
CC or in cell transplants. Up-regulation of the gene can also be used to  
CC modify cell lines cultured in vivo, e.g. to develop new lines, to  
CC facilitate isolation of hybridomas and to increase survival of primary  
CC explants during genetic modification. It can be used to produce  
CC recombinant Bcl-w for therapy, diagnosis, antibody production or  
CC screening of potential modulators.

XX SQ Sequence 168 AA;  
Query Match 86.1%; Score 867; DB 18; Length 168;  
Best Local Similarity 95.8%; Pred. No. 9.1e-88;  
Matches 161; Conservative 5; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFVGYKLQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MPTPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTPGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAAQLHVTPGSAQQORFTQVSDLELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120







ABG95556  
ID ABG95556 standard; Protein; 365 AA.  
XX  
AC ABG95556;  
XX  
DT 15-JAN-2003 (first entry)  
XX  
DE Human novel secreted protein gene 120 polypeptide #1.  
XX  
KW Human; secreted protein; autoimmune disease; chemotaxis;  
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasm;  
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis; sunburn;  
KW nervous system disorders; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing; tissue regeneration;  
KW epithelial cell proliferation; organ transplantation; food additive;  
KW preservative; nutritional.  
XX  
OS Homo sapiens.  
XX  
PN US6420526-B1.  
XX  
PD 16-JUL-2002.  
XX  
PF 08-SEP-1998; 98US-0149476.  
XX  
PR 07-MAR-1997; 97US-038621P.  
PR 07-MAR-1997; 97US-040161P.  
PR 07-MAR-1997; 97US-040162P.  
PR 07-MAR-1997; 97US-040163P.  
PR 07-MAR-1997; 97US-040333P.  
PR 07-MAR-1997; 97US-040334P.  
PR 07-MAR-1997; 97US-040336P.  
PR 07-MAR-1997; 97US-040626P.  
PR 11-APR-1997; 97US-043311P.  
PR 11-APR-1997; 97US-043312P.  
PR 11-APR-1997; 97US-043313P.  
PR 11-APR-1997; 97US-043314P.  
PR 11-APR-1997; 97US-043315P.  
PR 11-APR-1997; 97US-043568P.  
PR 11-APR-1997; 97US-043569P.  
PR 11-APR-1997; 97US-043576P.  
PR 11-APR-1997; 97US-043578P.  
R 11-APR-1997; 97US-043580P.  
R 11-APR-1997; 97US-043669P.  
PR 11-APR-1997; 97US-043670P.  
PR 11-APR-1997; 97US-043671P.  
PR 11-APR-1997; 97US-043672P.  
PR 11-APR-1997; 97US-043674P.  
PR 23-MAY-1997; 97US-047492P.  
PR 23-MAY-1997; 97US-047500P.  
PR 23-MAY-1997; 97US-047501P.  
PR 23-MAY-1997; 97US-047502P.  
PR 23-MAY-1997; 97US-047503P.  
PR 23-MAY-1997; 97US-047581P.  
PR 23-MAY-1997; 97US-047582P.  
PR 23-MAY-1997; 97US-047583P.  
PR 23-MAY-1997; 97US-047584P.  
PR 23-MAY-1997; 97US-047585P.  
PR 23-MAY-1997; 97US-047586P.  
PR 23-MAY-1997; 97US-047587P.  
PR 23-MAY-1997; 97US-047588P.  
PR 23-MAY-1997; 97US-047589P.  
PR 23-MAY-1997; 97US-047590P.  
PR 23-MAY-1997; 97US-047592P.  
PR 23-MAY-1997; 97US-047593P.  
PR 23-MAY-1997; 97US-047594P.  
PR 23-MAY-1997; 97US-047595P.  
R 23-MAY-1997; 97US-047596P.  
R 23-MAY-1997; 97US-047597P.  
R 23-MAY-1997; 97US-047598P.  
R 23-MAY-1997; 97US-047599P.  
R 23-MAY-1997; 97US-047600P.

PR 23-MAY-1997; 97US-047601P.  
PR 23-MAY-1997; 97US-047612P.  
PR 23-MAY-1997; 97US-047613P.  
PR 23-MAY-1997; 97US-047614P.  
PR 23-MAY-1997; 97US-047615P.  
PR 23-MAY-1997; 97US-047617P.  
PR 23-MAY-1997; 97US-047618P.  
PR 23-MAY-1997; 97US-047632P.  
PR 23-MAY-1997; 97US-047633P.  
PR 06-JUN-1997; 97US-048964P.  
PR 06-JUN-1997; 97US-048974P.  
PR 13-JUN-1997; 97US-049610P.  
PR 08-JUL-1997; 97US-051926P.  
PR 16-JUL-1997; 97US-052874P.  
PR 18-AUG-1997; 97US-055724P.  
PR 22-AUG-1997; 97US-056630P.  
PR 22-AUG-1997; 97US-056631P.  
PR 22-AUG-1997; 97US-056632P.  
PR 22-AUG-1997; 97US-056636P.  
PR 22-AUG-1997; 97US-056637P.  
PR 22-AUG-1997; 97US-056662P.  
PR 22-AUG-1997; 97US-056664P.  
PR 22-AUG-1997; 97US-056845P.  
PR 22-AUG-1997; 97US-056862P.  
PR 22-AUG-1997; 97US-056864P.  
PR 22-AUG-1997; 97US-056872P.  
PR 22-AUG-1997; 97US-056874P.  
PR 22-AUG-1997; 97US-056875P.  
PR 22-AUG-1997; 97US-056876P.  
PR 22-AUG-1997; 97US-056877P.  
PR 22-AUG-1997; 97US-056878P.  
PR 22-AUG-1997; 97US-056879P.  
PR 22-AUG-1997; 97US-056880P.  
PR 22-AUG-1997; 97US-056881P.  
PR 22-AUG-1997; 97US-056882P.  
PR 22-AUG-1997; 97US-056884P.  
PR 22-AUG-1997; 97US-056886P.  
PR 22-AUG-1997; 97US-056887P.  
PR 22-AUG-1997; 97US-056888P.  
PR 22-AUG-1997; 97US-056889P.  
PR 22-AUG-1997; 97US-056892P.  
PR 22-AUG-1997; 97US-056893P.  
PR 22-AUG-1997; 97US-056894P.  
PR 22-AUG-1997; 97US-056903P.  
PR 22-AUG-1997; 97US-056908P.  
PR 22-AUG-1997; 97US-056909P.  
PR 22-AUG-1997; 97US-056910P.  
PR 22-AUG-1997; 97US-056911P.  
PR 22-AUG-1997; 97US-057761P.  
PR 05-SEP-1997; 97US-057650P.  
PR 05-SEP-1997; 97US-057669P.  
PR 12-SEP-1997; 97US-058785P.  
PR 02-OCT-1997; 97US-061060P.  
PR 06-MAR-1998; 98WO-US04493.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
DR WPI; 2002-634796/68.  
XX  
PT New isolated human secreted protein for diagnosing, preventing,  
PT treating or ameliorating medical conditions and used as a food additive  
PT or preservative -  
XX  
PS Disclosure; Column 103; 129pp; English.  
XX  
CC The invention relates to an isolated protein that is one of 186 human  
CC secreted proteins, given in the specification, encoded by one of  
CC 309 cDNA sequences also given in the specification. The protein is used

CC in a pharmaceutical composition used to prevent, treat or ameliorate a  
CC medical condition in e.g. humans, mice, rabbits, goats, horses, cats,  
CC dogs, chickens or sheep. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease,  
CC infections caused by bacteria, viruses and fungi and ocular disorders  
CC e.g. corneal infection. The polypeptides can also be used to aid wound  
CC healing and epithelial cell proliferation, to prevent skin aging due to  
CC sunburn, to maintain organs before transplantation, for supporting cell  
CC culture of primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
CC carbohydrate, vitamins, minerals, cofactors and other nutritional  
CC components. The present sequence represents one of the novel human  
CC secreted proteins of the invention.

XX

SQ Sequence 365 AA;

Query Match 76.1%; Score 766; DB 23; Length 365;  
Best Local Similarity 100.0%; Pred. No. 4.1e-76;  
Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT	60
Db	1	MATPASAPDTRALVADFVGYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT	60
Qy	61	FSDLAAQLHVTGPSAQQRFTQVSDLELFQGGPNWGRLVAFVFGAALCAESVKNEMEPLVG	120
Db	61	FSDLAAQLHVTGPSAQQRFTQVSDLELFQGGPNWGRLVAFVFGAALCAESVKNEMEPLVG	120
Qy	121	QVQEWNVAYLETRLADWIHSSGGW	144
Db	121	QVQEWNVAYLETRLADWIHSSGGW	144

Search completed: October 24, 2003, 10:48:54  
Job time : 63 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 24, 2003, 10:46:25 ; Search time 21 Seconds  
(without alignments)  
388.857 Million cell updates/sec

Title: US-09-925-674A-7  
Perfect score: 1007  
Sequence: 1 MATPASAPDTRALVADFGV.....LTGAVALGALVTVGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA: \*  
1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1002	99.5	193	1	US-08-798-897-4
2	1002	99.5	193	2	US-08-978-523-4
3	997	99.0	192	1	US-08-798-897-6
4	997	99.0	192	2	US-08-978-523-6
5	996	98.9	193	1	US-08-798-897-3
6	996	98.9	193	2	US-08-978-523-3
7	991	98.4	192	1	US-08-798-897-5
8	991	98.4	192	2	US-08-978-523-5
9	766	76.1	365	4	US-09-149-476-696
10	429.5	42.7	233	4	US-09-271-014A-6
11	428.5	42.6	233	1	US-08-333-565-59
12	428.5	42.6	233	1	US-08-081-448-6
13	428.5	42.6	233	1	US-08-607-269-24
14	428.5	42.6	233	1	US-08-471-058-14
15	428.5	42.6	233	2	US-08-661-479-59
16	428.5	42.6	233	2	US-08-470-670A-7
17	428.5	42.6	233	3	US-08-471-057-14
18	428.5	42.6	233	3	US-08-481-739-2
19	428.5	42.6	233	3	US-09-167-921-2
20	428.5	42.6	233	3	US-09-323-743-2
21	428.5	42.6	233	4	US-08-461-511A-7
22	428.5	42.6	233	4	US-08-470-865-14
23	428.5	42.6	233	5	PCT-US94-07089-7
24	428.5	42.6	233	5	PCT-US95-04600-24
25	425	42.2	225	3	US-09-101-519-1
26	423.5	42.1	233	1	US-08-607-269-23
27	423.5	42.1	233	5	PCT-US95-04600-23

28	413	41.0	236	1	US-08-607-269-22	Sequence 22, Appl
29	413	41.0	236	3	US-09-127-048-9	Sequence 9, Appl
30	413	41.0	236	5	PCT-US95-04600-22	Sequence 22, Appl
31	412.5	41.0	239	1	US-08-112-208C-10	Sequence 10, Appl
32	412.5	41.0	239	1	US-08-248-819A-10	Sequence 10, Appl
33	412.5	41.0	239	2	US-08-337-646A-10	Sequence 10, Appl
34	412.5	41.0	239	2	US-08-856-531-10	Sequence 10, Appl
35	412.5	41.0	239	2	US-08-856-034-10	Sequence 10, Appl
36	412.5	41.0	239	3	US-09-127-048-8	Sequence 8, Appl
37	412.5	41.0	239	3	US-08-927-326-10	Sequence 10, Appl
38	412.5	41.0	239	4	US-09-379-820A-10	Sequence 10, Appl
39	410.5	40.8	239	1	US-08-333-565-51	Sequence 51, Appl
40	410.5	40.8	239	1	US-08-248-819A-12	Sequence 12, Appl
41	410.5	40.8	239	1	US-08-607-269-20	Sequence 20, Appl
42	410.5	40.8	239	1	US-08-471-058-12	Sequence 12, Appl
43	410.5	40.8	239	1	US-08-690-095-4	Sequence 4, Appl
44	410.5	40.8	239	2	US-08-465-485A-21	Sequence 21, Appl
45	410.5	40.8	239	2	US-08-661-479-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1  
US-08-798-897-4  
; Sequence 4, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.C.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-4

Query Match 99.5%; Score 1002; DB 1; Length 193;  
Best Local Similarity 99.5%; Pred. No. 6.9e-107;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Dd	1	MATPASAPDTRALVEDFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETFRRT	60
Qy	61	FSDLAAQLHVTGSAQQRFTQVSDLELFGGPNWGRLVAFVFFGAALCAESVKNEMEPLVG	120

Db 61 FSDLAQLHVTGSAQQRFTQVSDLELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
Db 121 QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
Db 181 GALVTVGAFPAASK 193

RESULT 2  
US-08-978-523-4  
; Sequence 4, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-978-523-4

Query Match 99.5%; Score 1002; DB 2; Length 193;  
Best Local Similarity 99.5%; Pred. No. 6.9e-107;  
Matches 192; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVEDFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGSAQQRFTQVSDLELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAQLHVTGSAQQRFTQVSDLELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
Db 121 QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180

QY 181 GALVTVGAFPAASK 193  
Db 181 GALVTVGAFPAASK 193  
RESULT 3  
US-08-798-897-6  
; Sequence 6, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-6

Query Match 99.0%; Score 997; DB 1; Length 192;  
Best Local Similarity 99.5%; Pred. No. 2.6e-106;  
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 ATPASAPDTRALVEDFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAQLHVTGSAQQRFTQVSDLELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 121  
Db 61 SDLAQLHVTGSAQQRFTQVSDLELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 120  
QY 122 QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALG 181  
Db 121 QVQEWNVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALG 180  
QY 182 ALVTVGAFPAASK 193  
Db 181 ALVTVGAFPAASK 192

RESULT 4  
US-08-978-523-6  
; Sequence 6, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John

; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-978-523-6
Query Match 99.0%; Score 997; DB 2; Length 192;
Best Local Similarity 99.5%; Pred. No. 2.6e-106;
Matches 191; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 ATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 61
Db 1 ATPASAPDTRALVEDFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 60
QY 62 SDLAAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEYEPLVGQ 121
Db 61 SDLAAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEYEPLVGQ 120
QY 122 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWASVRTVLTGAVALG 181
Db 121 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWASVRTVLTGAVALG 180
QY 182 ALVTVGAF FASK 193
Db 181 ALVTVGAF FASK 192
RESULT 5
US-08-978-897-3
; Sequence 3, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington

; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-798-897-3
Query Match 98.9%; Score 996; DB 1; Length 193;
Best Local Similarity 98.4%; Pred. No. 3.4e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
Db 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60
QY 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEYEPLVG 120
Db 61 FSDLAQLHVTGPSAQORFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEYEPLVG 120
QY 121 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWASVRTVLTGAVAL 180
Db 121 VQODMWVYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWASVRTVLTGAVAL 180
QY 181 GALVTVGAF FASK 193
Db 181 GALVTVGAF FASK 193
RESULT 6
US-08-978-523-3
; Sequence 3, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith



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; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-978-523-3

Query Match      98.9%; Score 996; DB 2; Length 193;
Best Local Similarity 98.4%; Pred. No. 3.4e-106;
Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 MATPASTPTDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 FSDLAALQHLVTPGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 QVQEMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWAASVRTVLTGAVAL 180
   |||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 QVQDMVVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWAASVRTVLTGAVAL 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 GALVTVGGAFFASK 193
   ||||| ||||| |||||
Db 181 GALVTVGGAFFASK 193
   ||||| ||||| |||||

RESULT 7
US-08-798-897-5
; Sequence 5, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DCS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600

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; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-798-897-5

Query Match      98.4%; Score 991; DB 1; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 ATPASTPTDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 SDLAAQLHVTGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVGQ 121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SDLAAQLHVTGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVGQ 120
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QY 122 VQEMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWAASVRTVLTGAVALG 181
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Db 121 VQDMVVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWAASVRTVLTGAVALG 180
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QY 182 ALVTVGGAFFASK 193
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Db 181 ALVTVGGAFFASK 192
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RESULT 8
US-08-978-523-5
; Sequence 5, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 192 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear

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; MOLECULE TYPE: protein
US-08-978-523-5
Query Match: 98.4%; Score 991; DB 2; Length 192;
Best Local Similarity 98.4%; Pred. No. 1.2e-105;
Matches 189; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61
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Db 1 ATPASTPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 SDLAAQLHVTGSAQORFTQVSDELFGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVQ 121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SDLAAQLHVTGSAQORFTQVSDELFGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVQ 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 122 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGALAEARLRREGNWASVRTVLTGAVALG 181
   ||:|||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 VQDWMTVYLETRLADWIHSSGGWAEFTALYGDGALAEARLRREGNWASVRTVLTGAVALG 180
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QY 182 ALVTVGAFASK 193
   ||||| ||||| |||||
Db 181 ALVTVGAFASK 192
   ||||| ||||| |||||

RESULT 9
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,617
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,503
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,592
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,581
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,500
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,587
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,613
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,580
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,568
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,314
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,569
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,311
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,313
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,672
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,315
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,662
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,872
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,903
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
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; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/333,565
; FILING DATE: 31-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; US-08-333-565-59

Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 41.3%; Pred. No. 5.1e-41;
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

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QY 29 CGAGPGEPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAALHVTGSAQQRFT 80
Db 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
QY 81 QVSELFQGGPNWGRIVAFFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWIHS 140
Db 125 QVWNELFRDGVNWRIVAFFSFGGALCVESVDKEMQVLVSRIAAMMATYLNHLEPWIQE 184
QY 141 SGGWAEFTALYGDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
Db 185 NGGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVVJLGSJ 229

RESULT 12
US-08-081-448-6
; Sequence 6, Application US/08081448
; Patent No. 5646008
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:
; TITLE OF INVENTION: Compositions and Methods
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: 321 No. 5646008th Clark Street, Suite 800
; CITY: Chicago
; STATE: IL
; COUNTRY: USA
; ZIP: 60610
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,448
; FILING DATE: 19930622
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 5646008thrup, Thomas E.
; REGISTRATION NUMBER: 33,268
; REFERENCE/DOCKET NUMBER: ARCD090
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-744-0090
; TELEFAX: 312-755-4489
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-081-448-6

Query Match 42.6%; Score 428.5; DB 1; Length 233;
Best Local Similarity 40.6%; Pred. No. 5.1e-41;
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;

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Db 6 RELVDFLSYKLSQKGSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALHVTGSAQQRFTQ 81
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125
QY 82 VSDELFQGGPNWGRIVAFFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWIHSS 141
Db 126 VVNELFRDGVNWRIVAFFSFGGALCVESVDKEMQVLVSRIAAMMATYLNHLEPWIQEN 185
QY 142 GGWAEFTALYGDGALEEARLRE--GNWASVRTVLTGAVALGAL 183
Db 186 GGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVVLLGSL 229

RESULT 13
US-06-607-269-24
; Sequence 24, Application US/08607269
; Patent No. 5702897
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Sato, Takaaki
; TITLE OF INVENTION: Interaction of Proteins Involved in a
; TITLE OF INVENTION: Cell Death Pathway
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/607,269
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/226,876
; FILING DATE: 13-APR-1994
; ATTORNEY/AGENT INFORMATION:





Query Match	42.6%	Score 428.5;	DB 2;	Length 233;
Best Local Similarity	41.3%	Pred. No. 5.1e-41;		
Matches	93;	Conservative 22;	Mismatches 57;	Indels 53; Gaps 4;

  

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Db	6	RELVDLFLSYKLSQKGYWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65
Qy	29	CGAGPGEGPAAD-----PLHQAMRAAGDEFFETRFRRTFSDLAAQLHVTGSSAQORFT 80
Db	66	NGA-TGHSSSLDAREVIPMAAVKQAJREAGDEFELRYRRAPFSDLTSQLHITPGTAYQSF 124
Qy	81	QVSDELFQGGPNWGRLLVAFVFGAALCAESVNKEMEPLVGQVQEWMMVAYLETRLADWHS 140
Db	125	QVNVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRIAAMMATYLNNDHLEPWIQ 184
Qy	141	SGGWAFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
Db	185	NGGWDTFVELYGNNAAAESRKQGERENRWFLTGMTVAGVVLLGSL 229

Search completed: October 24, 2003, 10:52:51  
Job time : 23 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on:           October 24, 2003, 10:51:15 ; Search time 45.5 Seconds  
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Title:           US-09-925-674A-7  
Perfect score:   1007  
Sequence:       1 MATPASAPDTRALVADFGY.....LTGAVALGALVTVGAFPAASK 193

Scoring table:   BLOSUM62  
                  Gapop 10.0 , Gapext 0.5

Searched:       629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters:       629382

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
                  Maximum Match 100%  
                  Listing first 45 summaries

Database :       Published Applications AA:\*

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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*

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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	766	76.1	365	12	US-09-882-171-696
5	428.5	42.6	233	9	US-09-734-846-2
6	428.5	42.6	233	10	US-09-952-278-6
7	428.5	42.6	233	12	US-10-169-223-10
8	428.5	42.6	233	12	US-10-302-262-2
9	428.5	42.6	233	15	US-10-101-482-14
10	428.5	42.6	233	15	US-10-072-830-4
11	415.5	41.3	152	15	US-10-158-769-2
12	412.5	41.0	239	15	US-10-277-693A-10
13	410.5	40.8	239	8	US-08-726-211-5
14	410.5	40.8	239	12	US-10-141-618-12
15	410.5	40.8	239	12	US-10-053-645A-21

16	410.5	40.8	239	15	US-10-101-482-12	Sequence 12, Appli
17	410.5	40.8	239	15	US-10-072-830-2	Sequence 2, Appli
18	406	40.3	236	15	US-10-277-693A-11	Sequence 11, Appli
19	401	39.8	212	12	US-10-169-223-14	Sequence 14, Appli
20	378	37.5	190	10	US-09-952-278-2	Sequence 2, Appli
21	374.5	37.2	235	15	US-10-208-155-2	Sequence 2, Appli
22	374	37.1	155	15	US-10-158-769-1	Sequence 1, Appli
23	373.5	37.1	185	9	US-09-864-761-40954	Sequence 40954, A
24	346	34.4	205	8	US-08-726-211-7	Sequence 7, Appli
25	346	34.4	205	10	US-09-952-278-4	Sequence 4, Appli
26	346	34.4	205	12	US-10-053-645A-23	Sequence 23, Appli
27	241	23.9	49	9	US-09-864-761-34213	Sequence 34213, A
28	205	20.4	63	10	US-09-952-278-3	Sequence 3, Appli
29	183	18.2	170	10	US-09-952-278-8	Sequence 8, Appli
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32	176	17.5	211	15	US-10-189-294-2	Sequence 2, Appli
33	176	17.5	211	15	US-10-177-293-25	Sequence 25, Appli
34	173	17.2	211	15	US-10-101-482-9	Sequence 9, Appli
35	173	17.2	211	15	US-10-101-482-11	Sequence 11, Appli
36	168.5	16.7	210	15	US-10-101-482-22	Sequence 22, Appli
37	155.5	15.4	192	15	US-10-277-693A-8	Sequence 8, Appli
38	153	15.2	191	15	US-10-196-793A-46	Sequence 46, Appli
39	153	15.2	192	12	US-10-306-878-5	Sequence 5, Appli
40	153	15.2	192	15	US-10-101-482-13	Sequence 13, Appli
41	153	15.2	192	15	US-10-277-693A-9	Sequence 9, Appli
42	153	15.2	331	9	US-09-033-525-2	Sequence 2, Appli
43	152	15.1	192	15	US-10-277-693A-2	Sequence 2, Appli
44	150	14.9	280	15	US-10-101-482-19	Sequence 19, Appli
45	149	14.8	117	15	US-10-189-294-4	Sequence 0, Appli

ALIGNMENTS

RESULT 1

US-09-925-674A-7

; Sequence 7, Application US/09925674A

; Patent No. US20020119943A1

; GENERAL INFORMATION:

; APPLICANT: AMRAD Operations Pty Ltd

; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2

; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES

; FILE REFERENCE: 11686a

; CURRENT APPLICATION NUMBER: US/09/925,674A

; CURRENT FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: 09/925,674

; PRIOR FILING DATE: 2001-08-09

; PRIOR APPLICATION NUMBER: PN8965

; PRIOR FILING DATE: 1996-03-27

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 7

; LENGTH: 193

; TYPE: PRT

; ORGANISM: HUMAN

US-09-925-674A-7

Query Match	100.0%;	Score	1007;	DB	10;	Length	193;
Best Local Similarity	100.0%;	Pred. No.	3.9e-102;				
Matches	193;	Conservative	0;	Mismatches	0;	Indels	0;
QY	1	MATPASAPDTRALVADFGYKLRQKGYCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT	60				
Db	1	MATPASAPDTRALVADFGYKLRQKGYCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT	60				
QY	61	FSDLAAQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG	120				
Db	61	FSDLAAQLHVTTPGSAQQRFTQVSDLEFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG	120				
QY	121	QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLRGNWASVRTVLTGAV	180				
Db	121	QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALBEARRLRGNWASVRTVLTGAV	180				

QY 181 GALVTVGAFASK 193  
| | | | |  
Db 181 GALVTVGAFASK 193

RESULT 2

US-09-925-674A-9  
; Sequence 9, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-925-674A-9

Query Match 99.0%; Score 997; DB 10; Length 193;  
Best Local Similarity 98.4%; Pred. No. 4.9e-101;  
Matches 190; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
| | | | |  
Db 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120  
| | | | |  
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120  
  
QY 121 QVOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLGTGAVAL 180  
| | | | |  
Db 121 QVOEWMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLGTGAVAL 180  
  
QY 181 GALVTVGAFASK 193  
| | | | |  
Db 181 GALVTVGAFASK 193

RESULT 3

US-09-809-391-696  
; Sequence 696, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 696  
; LENGTH: 365  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-809-391-696

Query Match 76.1%; Score 766; DB 11; Length 365;  
Best Local Similarity 100.0%; Pred. No. 2.3e-75;  
Matches 144; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
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Db 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120  
| | | | |  
Db 61 FSDLAALQHLVTPGSAQQRFTQVSDLELFQGGPNWGRLVAFFVFGAALCAESVNKEMEPLVG 120  
  
QY 121 QVOEWMVAYLETRLADWIHSSGGW 144  
| | | | |  
Db 121 QVOEWMVAYLETRLADWIHSSGGW 144

RESULT 4

US-09-882-171-696  
; Sequence 696, Application US/09882171  
; Publication No. US20030175858A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: PZ002P2  
; CURRENT APPLICATION NUMBER: US/09/882,171  
; CURRENT FILING DATE: 2001-06-18  
; PRIOR APPLICATION NUMBER: 09/809,391  
; PRIOR FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 09/149,476  
; PRIOR FILING DATE: 1998-09-08  
; PRIOR APPLICATION NUMBER: PCT/US98/04493  
; PRIOR FILING DATE: 1998-03-06  
; PRIOR APPLICATION NUMBER: 60/040,162  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,333  
; PRIOR FILING DATE: 1997-03-07  
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; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/040,163  
; PRIOR FILING DATE: 1997-03-07  
; PRIOR APPLICATION NUMBER: 60/047,600  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR APPLICATION NUMBER: 60/047,617  
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; PRIOR APPLICATION NUMBER: 60/047,618  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,503  
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; PRIOR APPLICATION NUMBER: 60/047,592  
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; PRIOR APPLICATION NUMBER: 60/047,500  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,587  
; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23

; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
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; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
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; PRIOR APPLICATION NUMBER: 60/043,670  
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; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match

Best Local Similarity 76.1%; Score 766; DB 12; Length 365;

Matches 144; Conservative 0; Mismatches 0; Indels 0; Gaps 0;









STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,211  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: UTXC:504  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-726-211-5

Query Match 40.8%; Score 410.5; DB 8; Length 239;  
Best Local Similarity 37.0%; Pred. No. 1.1e-36;  
Matches 87; Conservative 35; Mismatches 58; Indels 55; Gaps 5;  
QY 9 DTRALVADFVGKLRQKGYVCGAG-----PGE----- 35  
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Db 10 DNREIVMKYIHYKLSQRGYEWDAAGVGAAPGPAAPGIFSSQPGHTPHPAASRDVPART 69  
| | | | | : : : : : | | | | |  
QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAACLHVTPGSAQQR 78  
| | | | | : : : : : | | | | |  
Db 70 SPLQTPAAPGAAAGPALSPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGR 129  
| | | | | : : : : : | | | | |  
QY 79 FTQVSDLELFGGPNWGRVLAFFVFGAALCAESVNKEMEPLVGVQVQEWVAYLETRLADWI 138  
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Db 130 FATVVEELFRDGVNWGRIVAFVFFGGVMCVESVNREMSPLVDNIALWMTEYLNRRHLHTWI 189  
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QY 139 HSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALGALVTVGAFPAASK 193  
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Db 190 QDNGGWDADFVELYG---PSMRPLDFSWLSLKLTLALLAL-VGACITLGAYLSHK 239  
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RESULT 14  
US-10-141-618-12  
; Sequence 12, Application US/10141618  
; Publication No. US20030165887A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: Methods For Determining the Prognosis  
; FILE REFERENCE: P-LJ 5254  
; CURRENT APPLICATION NUMBER: US/10/141,618  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 60/289,233  
; PRIOR FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: US 60/356,934  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US 09/388,221  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-141-618-12  
Query Match 40.8%; Score 410.5; DB 12; Length 239;  
Best Local Similarity 37.0%; Pred. No. 1.1e-36;  
Matches 87; Conservative 35; Mismatches 58; Indels 55; Gaps 5;  
QY 9 DTRALVADFVGKLRQKGYVCGAG-----PGE----- 35  
| | | | | : : : : : | | | | |  
Db 10 DNREIVMKYIHYKLSQRGYEWDAAGVGAAPGPAAPGIFSSQPGHTPHPAASRDVPART 69  
| | | | | : : : : : | | | | |  
QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAACLHVTPGSAQQR 78  
| | | | | : : : : : | | | | |  
Db 70 SPLQTPAAPGAAAGPALSPVPPVHLLALRQAGDDFSRRYRGDFAEMSSQLHLTPFTARGR 129  
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QY 79 FTQVSDLELFGGPNWGRVLAFFVFGAALCAESVNKEMEPLVGVQVQEWVAYLETRLADWI 138  
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Db 130 FATVVEELFRDGVNWGRIVAFVFFGGVMCVESVNREMSPLVDNIALWMTEYLNRRHLHTWI 189  
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QY 139 HSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALGALVTVGAFPAASK 193  
| | | | | : : : : : | | | | |  
Db 190 QDNGGWDADFVELYG---PSMRPLDFSWLSLKLTLALLAL-VGACITLGAYLSHK 239  
| | | | | : : : : : | | | | |  
RESULT 15  
US-10-053-645A-21  
; Sequence 21, Application US/10053645A  
; Publication No. US20030176376A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert E. Klem  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A  
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2  
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF  
; FILE REFERENCE: 10412-022-999  
; CURRENT APPLICATION NUMBER: US/10/053,645A  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/263,244  
; PRIOR FILING DATE: 2001-01-22  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-053-645A-21

Query Match 40.8%; Score 410.5; DB 12; Length 239;  
Best Local Similarity 37.0%; Pred. No. 1.1e-36;  
Matches 87; Conservative 35; Mismatches 58; Indels 55; Gaps 5;  
QY 9 DTRALVADFVGKLRQKGYVCGAG-----PGE----- 35  
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Db 10 DNREIVMKYIHYKLSQRGYEWDAAGVGAAPGPAAPGIFSSQPGHTPHPAASRDVPART 69  
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QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAACLHVTPGSAQQR 78  
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QY 79 FTQVSDLELFGGPNWGRVLAFFVFGAALCAESVNKEMEPLVGVQVQEWVAYLETRLADWI 138  
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Db 130 FATVVEELFRDGVNWGRIVAFVFFGGVMCVESVNREMSPLVDNIALWMTEYLNRRHLHTWI 189  
| | | | | : : : : : | | | | |  
QY 139 HSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALGALVTVGAFPAASK 193  
| | | | | : : : : : | | | | |  
Db 190 QDNGGWDADFVELYG---PSMRPLDFSWLSLKLTLALLAL-VGACITLGAYLSHK 239  
| | | | | : : : : : | | | | |

Search completed: October 24, 2003, 11:04:40  
Job time : 47.5 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:44:00 ; Search time 25 Seconds  
(without alignments)  
742.422 Million cell updates/sec

Title: US-09-925-674A-7  
Perfect score: 1007  
Sequence: 1 MATPASAPDTRALVADFGY.....LTGAVALGALVTVGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	428.5	42.6	233	2 I49056	bcl-x long - mouse
2	428.5	42.6	233	2 B47537	apoptosis regulator
3	424.5	42.2	233	2 S51761	BCL-X protein - ra
4	423.5	42.1	233	2 A37332	transforming prote
5	414	41.1	232	2 S24390	transforming prote
6	412.5	41.0	239	1 TVHUA1	transforming prote
7	412	40.9	236	2 I67432	BCL-2 - rat (fragm
8	407	40.4	236	2 I53744	gene bcl-2 protein
9	406	40.3	236	1 TVMSA1	transforming prote
10	404.5	40.2	233	2 I67431	BCL-X-Long - ra:
11	403	40.0	236	2 JC7383	B-cell lymphoma 2
12	378	37.5	190	2 A47537	apoptosis regulato
13	377.5	37.5	214	2 I49057	bcl-x transmembran
14	375.5	37.3	227	2 JEO203	apoptosis regulato
15	356	35.4	216	2 B37332	transforming prote
16	349.5	34.7	199	1 TVMSB1	transforming prote
17	346	34.4	205	1 TVHUB1	transforming prote
18	277.5	27.6	154	2 I58194	gene bcl-2 protein
19	182	18.1	170	2 I49055	bcl-x short - mous
20	176	17.5	211	2 S58873	Bak protein - huma
21	174	17.3	176	2 I67435	gene bcl-xshort pr
22	173	17.2	211	2 S58875	cdn-2 protein - fu
23	157.5	15.6	192	2 D47538	bcl-2-associated p
24	153	15.2	192	2 A47538	bcl-2-associated p
25	150	14.9	261	2 H88578	protein ced-9 limp
26	150	14.9	280	2 A53189	apoptosis suppress
27	149.5	14.8	133	2 I53295	bcl-2-associated p
28	146.5	14.5	179	2 JC7255	Bax-delta protein
29	146.5	14.5	218	2 B47538	bcl-2-associated p

30	143	14.2	177	2 S54778	NR-13 protein - qu
31	141	14.0	255	2 JC7567	Mcl-1a protein - z
32	137.5	13.7	143	2 I38921	bcl-2-associated p
33	118	11.7	175	2 I39055	Bcl-2 related - hu
34	112	11.1	350	2 A47476	BCL2 homolog MCL1
35	105	10.4	172	2 I49449	hemopoietic-specif
36	91.5	9.1	301	2 T36534	probable lipase/es
37	89	8.8	185	2 B83217	hypothetical prote
38	87	8.6	3433	1 GNWVKV	genome polyprotein
39	85	8.4	270	2 AI2598	dihydrodipicolinat
40	85	8.4	279	2 B97381	dihydrodipicolinat
41	84.5	8.4	358	1 AJLCQB	glutamate-ammonia
42	83	8.2	417	2 T39939	DNA binding protei
43	82.5	8.2	1440	1 GNWVJF	genome polyprotein
44	82.5	8.2	3432	1 GNWVJE	genome polyprotein
45	81.5	8.1	354	2 S52040	Glr 1.1 protein -

ALIGNMENTS

RESULT 1  
I49056  
bcl-x long - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C;Accession: I49056; S52866  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A;Accession: I49056  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: EMBL:U10101; NID:G506647; PIDN:AAA82173.1; PID:G506648  
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line thr  
A;Reference number: S52866  
A;Accession: S52866  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-233 <KAM>  
A;Cross-references: EMBL:X83574; NID:G695622; PIDN:CAA58557.1; PID:G695623  
C;Superfamily: bcl transforming protein

Query Match 42.6%; Score 428.5; DB 2; Length 233;  
Best Local Similarity 41.3%; Pred. No. 2.8e-32;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

Cy	11	RALVADFGYKLRQGY-----	-----V 28
Db	6	RELVDVFLSYKLSQKYSWSQFS	SDVEENRTEAPEETEAEETPSAINGNPSWHLADSPAV 65
Cy	29	CGAGPGECPAAD-----	PLHQAMRAAGDEFETRFRRTFSDLAAQLHVTTPGSAQQRFT 80
Db	66	NGA-TGHSSSLDAREVIPMAAV	KQALREAGDEFELRYRRAFSDLTSQLHITPTGTAYQSFE 124
Cy	81	QVSDelfQGGPNWGRLVAF	FFVFGAALCAESVNMKEMEPLVGQVQEWVMVAYLETRLADWIHS 140
Db	125	QVNVNELFRDGVNWGRIVAF	FFSFGGALCVESVDKEMQVLSRIASWMTYLNHDHLEPWIOE 184
Cy	141	SGGWAETALYGDGALAEARR	LR--GNWASVRTVLTGAVALLGAL 183
Db	185	NGGWDTFVDLYGNNAAESRK	QERFNRWFLTGMTVAGVWLLGSL 229

RESULT 2  
B47537  
apoptosis regulator bcl-xL - human  
N;Alternate names: bcl-2-related protein  
N;Contains: apoptosis regulator bcl-xs



C;Species: Homo sapiens (man)  
C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Jul-1999  
C;Accession: B47537; C47537  
R;Boise, L.H.; Gonzalez-Garcia, M.; Postema, C.E.; Ding, L.; Lindsten, T.; Turka, L.A.;  
Cell 74, 597-608, 1993  
A;Title: bcl-x, a bcl-2-related gene that functions as a dominant regulator of apoptotic  
A;Reference number: A47537; MUID:93364977; PMID:8358789  
A;Accession: B47537  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <BO1>  
A;Cross-references: GB:L20121; NID:g510900; PIDN:CAA80661.1; PID:g510901  
A;Accession: C47537  
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-69, 'G', 71-125, 189-233 <BO2>  
A;Cross-references: GB:L20122; NID:g623236; PIDN:CAA80662.1; PID:g623237  
C;Genetics:  
A;Gene: GDB:BCL2L  
A;Cross-references: GDB:228079  
C;Superfamily: bcl transforming protein  
C;Keywords: alternative splicing; apoptosis  
F;1-233/Product: apoptosis regulator bcl-xL #status predicted <MAT>  
F;1-125,189-233/Product: apoptosis regulator bcl-xS #status predicted <MA2>  
  
Query Match 42.6%; Score 428.5; DB 2; Length 233;  
Best Local Similarity 40.6%; Pred. No. 2.8e-32;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;  
  
QY 11 RLVADFVGYKLRQKGY-----PLHQAMRAAGDEFETFRRTFSDLAAQLHVTTPGSAQQRFTQ 39  
Db 6 RELVDFLSYKLSQKYSWSQFSDFVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65  
  
QY 40 D-----PLHQAMRAAGDEFETFRRTFSDLAAQLHVTTPGSAQQRFTQ 81  
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFEQ 125  
  
QY 82 VSEDLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEMMVAYLETRLADWIHSS 141  
Db 126 VVNELFRDGVNWGRIVAFVFGGALCVESVDKEMQVLSRIASMMATYLNCHLEPWIQEN 185  
  
QY 142 GGWAEFTALYGDGALEEARLRE--GNWASVRTVLTGAVAGAL 183  
Db 186 GGWDTFVELYGNNAAEASRKQGERFNRWFLTGMTVAGVLLGSL 229  
  
RESULT 3  
S51761  
BCL-X protein - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 02-Mar-2001  
C;Accession: S51761; S51762  
R;Michaelidis, T.M.  
submitted to the EMBL Data Library, November 1994  
A;Reference number: S51761  
A;Accession: S51761  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-233 <MIC>  
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57886.1; PID:g607177  
A;Experimental source: embryonic; brain  
A;Accession: S51762  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-125,189-233 <MI2>  
A;Cross-references: EMBL:X82537; NID:g607176; PIDN:CAA57887.1; PID:g607178  
A;Experimental source: embryonic; brain  
A;Note: smaller form due to splicing  
C;Genetics:  
A;Introns: 125/3  
C;Superfamily: bcl transforming protein  
  
Query Match 42.2%; Score 424.5; DB 2; Length 233;

Best Local Similarity 41.3%; Pred. No. 6.5e-32;  
Matches 92; Conservative 22; Mismatches 56; Indels 53; Gaps 4;  
  
QY 13 LRVADFVGYKLRQKGY-----PLHQAMRAAGDEFETFRRTFSDLAAQLHVTTPGSAQQRFTQV 30  
Db 8 LRVDFLSYKLSQKYSWSQFSDFVEENRTEAPEETEPEPTPSAINGNPSWHLADS?AVNG 67  
  
QY 31 AGPGEPPAAD-----PLHQAMRAAGDEFETFRRTFSDLAAQLHVTTPGSAQQRFTQV 82  
Db 68 A-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTPTGTAYQSFEQV 126  
  
QY 83 SDELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEMMVAYLETRLADWIHSSG 142  
Db 127 VNELFRDGVNWGRIVAFVFGGALCVESVDKEMQVLSRIASMMATYLNCHLEPWIQENG 186  
  
QY 143 GWAFTALYGDGALEEARLRE--GNWASVRTVLTGAVAGAL 183  
Db 187 GWDTFVDLYGNNAAEASRKQGERFNRWFLTGMTVAGVLLGSL 229  
  
RESULT 4  
A37332  
transforming protein (bcl-2-alpha) - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 23-Feb-1997  
C;Accession: A37332; S35453  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a var  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: A37332  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-233 <EGU>  
A;Cross-references: EMBL:D11381  
C;Genetics:  
A;Introns: 189/3  
C;Superfamily: bcl transforming protein  
C;Keywords: mitochondrion; transforming protein; transmembrane protein  
  
Query Match 42.1%; Score 423.5; DB 2; Length 233;  
Best Local Similarity 38.0%; Pred. No. 8.1e-32;  
Matches 87; Conservative 32; Mismatches 61; Indels 49; Gaps 4;  
  
QY 9 DTRALVADFVGYKLRQKYSVCGAG-----PGESPAAADP----- 41  
Db 10 DNREIVLKYIHYKLSQSGYDWAAGDRPPVPAPAPAPAAAAAAGASSHHRPEPPGSA 69  
  
QY 42 -----LHQAMRAAGDEFETFRRTFSDLAAQLHVTTPGSAQQRFTQVSD 84  
Db 70 AASEVPPAEGLRPAPPGVHLALRQAGDEFRRRYQDFQMSGQLHTPTTAHGRFVAVVE 129  
  
QY 85 ELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEMMVAYLETRLADWIHSSGGW 144  
Db 130 ELFRDGVNWGRIVAFVFGGVMCVESVNREMSPLVDNIATMTTEYLNRHLHNWIQDNGGW 189  
  
QY 145 AEFTALYGDGALEEARLREGNWSVRTVLTGAVAGALVTVGAFASK 193  
Db 190 DAFVELYGN----SMRPLDFSWISLKTILS-LVLVGACITLGAYLGHK 233  
  
RESULT 5  
S24390  
transforming protein (Bcl-2) homolog - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 16-Jul-1999  
C;Accession: S24390  
R;Cazals-Hatem, D.L.; Louie, D.C.; Tanaka, S.; Reed, J.C.  
Biochim. Biophys. Acta 1132, 109-113, 1992  
A;Title: Molecular cloning and DNA sequence analysis of cDNA encoding chicken homolog  
A;Reference number: S24390; MUID:92379084; PMID:1511008  
A;Accession: S24390  
A;Status: preliminary



A;Molecule type: mRNA  
A;Residues: 1-232 <CA2>  
A;Cross-references: EMBL:Z11961; NID:G62969; PIDN:CAA78018.1; PID:G62970  
C;Superfamily: bcl transforming protein  
C;Keywords: mitochondrion; transmembrane protein

Query Match 41.1%; Score 414; DB 2; Length 232;  
Best Local Similarity 37.7%; Pred. No. 6.1e-31;  
Matches 86; Conservative 32; Mismatches 62; Indels 48; Gaps 4;

QY 9 DTRALVADFVGKLRQKGYVCGAG-----PGEPPAADP----- 41  
Db 10 DNREIVLKYIHYKLSQRGYDWAAGEDRPVPVPAPAPAAAPAAVAAAGASSHHRPSPPARL 69

QY 42 -----LHQAMRAAGDEFETFRFRRTFSDLAAQLHVTFGSAQQRFQVSDE 85  
Db 70 LLVRCPLRGCAAPPGVHIALRQAGDEFRRYQDFQAQMSGQLHLPFTATGRFVAVVEE 129

QY 86 LFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWIHSSGGWA 145  
Db 130 LFRDGVNWVRIVAFVFGGVCMCVSNREMSPLVDNIATWMTTEYLNRHLHNWIQDNGGWD 189

QY 146 EFTALYGDGALEEARLRREGNWSVRTVLTGVALGALVTVGAFPAASK 193  
Db 190 AFVELYGN-----SMRPLDFSWISLKTILS-LVLVGACITLGAYLGHK 232

RESULT 6  
TVHUAL  
transforming protein bcl-2, splice form alpha - human  
C;Species: Homo sapiens (man)  
C;Date: 31-Dec-1988 #sequence\_revision 07-Jun-1996 #text\_change 15-Oct-1999  
C;Accession: C37332; A29409; S02452; A24428; A27622; B27622  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: C37332  
A;Status: nucleic acid sequence not shown; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-239 <EGU>  
A;Note: this report is a correction  
R;Tsujimoto, Y.; Croce, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 83, 5214-5218, 1986  
A;Title: Analysis of the structure, transcripts, and protein products of bcl-2, the gene for the B-cell lymphoma cell line BL2  
A;Reference number: A29409; MUID:86259760; PMID:3523487  
A;Accession: A29409  
A;Molecule type: mRNA  
A;Residues: 1-95, 'A', 97-109, 'G', 111-236, 'S', 238-239 <TSU>  
A;Cross-references: GB:M13994; NID:G179366; PIDN:AAA51813.1; PID:G179367  
A;Note: this sequence has been corrected in reference A37332  
R;Seto, M.; Jaeger, U.; Hockett, R.D.; Graninger, W.; Bennett, S.; Goldman, P.; Korsmeyer, S.J.  
EMBO J. 7, 123-131, 1988  
A;Title: Alternative promoters and exons, somatic mutation and deregulation of the Bcl-2 gene in human B-cell lymphomas  
A;Reference number: S02452; MUID:88196071; PMID:2834197  
A;Accession: S02452  
A;Molecule type: mRNA  
A;Residues: 1-239 <SET>  
R;Cleary, M.L.; Smith, S.D.; Sklar, J.  
Cell 47, 19-28, 1986  
A;Title: Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-2/immunoglobulin heavy chain enhancer  
A;Reference number: A24428; MUID:87002488; PMID:2875799  
A;Accession: A24428  
A;Molecule type: mRNA  
A;Residues: 1-58, 'T', 60-116, 'R', 118-239 <CLE>  
A;Cross-references: GB:M14745; NID:G179370; PIDN:AAA35591.1; PID:G179371  
R;Hua, C.; Zorn, S.; Jensen, J.P.; Coupland, R.W.; Ko, H.S.; Bakhshi, A.  
Oncogene Res. 2, 263-275, 1988  
A;Title: Consequences of the t(14;18) chromosomal translocation in follicular lymphoma: evidence for a bcl-2 gene breakpoint on chromosome 2  
A;Reference number: A27622; MUID:88217344; PMID:3285301  
A;Accession: A27622  
A;Molecule type: mRNA  
A;Residues: 1-58, 'T', 60-239 <HUA>

A;Accession: B27622  
A;Molecule type: DNA  
A;Residues: 1-6, 'S', 8-58, 'T', 60-128, 'C', 130-239 <HUA2>  
A;Note: the sequence was determined from the germline gene  
C;Comment: Constitutive expression of BCL2 following t(14;18) chromosomal translocation  
C;Genetics:  
A;Gene: GDB:BCL2  
A;Cross-references: GDB:119031; OMIM:151430  
A;Map position: 18q21.3-18q21.3  
C;Function:  
A;Description: blocks apoptosis in hematopoietic cells  
C;Superfamily: bcl transforming protein  
C;Keywords: alternative splicing; apoptosis; B-cell lymphoma; follicular lymphoma; pre-B-cell leukemia

Query Match 41.0%; Score 412.5; DB 1; Length 239;  
Best Local Similarity 37.0%; Pred. No. 8.7e-31;  
Matches 87; Conservative 34; Mismatches 59; Indels 55; Gaps 5;

QY 9 DTRALVADFVGKLRQKGYVCGAG-----PGE----- 35  
Db 10 DNREIVMKYIHYKLSQRGYEWDAGDVGAAPPGAAPAPGIPSSQPGHTPHPAASRDPVART 69

QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAAQLHVTTPGSAQQR 78  
Db 70 SPLQTPAAPGAAGPALSPPVPVHLTLRQAGDDFSRRYRRDFAEMSSQLHLPFTARGR 129

QY 79 FTQVSDLELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWI 138  
Db 130 FATVVEELFRDGVNWGRIVAFVFGGVCMCVSNREMSPLVDNIALWMTTEYLNRHLHTWI 189

QY 139 HSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGVALGALVTVGAFPAASK 193  
Db 190 QDNGGWDAFVELYG----PSMRPLDFSWLSLKTLLSLAL-VGACITLGAYLGHK 239

RESULT 7  
I67432  
BCL-2 - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Jul-1999  
C;Accession: I67432  
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.  
Endocrinology 136, 232-241, 1995  
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi-  
onstitutive bcl-2 and bcl-xiong messenger ribonucleic acid levels.  
A;Reference number: I53295; MUID:95129487; PMID:7828536  
A;Accession: I67432  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-236 <RES>  
A;Cross-references: EMBL:U34964; NID:G1004378; PIDN:AAA77687.1; PID:G1004379  
C;Superfamily: bcl transforming protein

Query Match 40.9%; Score 412; DB 2; Length 236;  
Best Local Similarity 36.2%; Pred. No. 9.6e-31;  
Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

QY 9 DTRALVADFVGKLRQKGY----- 27  
Db 10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAPTGFISFQPSNRTPAVERDTAART 69

QY 28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETFRFRRTFSDLAAQLHVTTPGSAQQRFQ 81  
Db 70 SPLRPLVANAGPALSPPVPVHLTLRAGDDFSRRYRRDFAEMSSQLHLPFTARGFAT 129

QY 82 VSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNWGRIVAFVFGGVCMCVSNREMYPLVDNIALWMTTEYLNRHLHTWIQDN 189

QY 142 GGWAEFTALYGDGALEEARLRREGNWSVRTVLTGVALGALVTVGAFPAASK 193  
Db 190 GGWDADFVELYG----PSMRPLDFSWQSLKTLLSLAL-VGACITLGAYLGHK 236

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RESULT 8
153744
gene bcl-2 protein - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C:Accession: 153744
R:Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A:Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A:Reference number: 153744; MUID:94193015; PMID:8144041
A:Accession: 153744
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-236 <RES>
A:Cross-references: GB:L14680; NID:G408946; PIDN:AAA3662.1; PID:G408947
C:Genetics:
A:Gene: bcl-2
C:Superfamily: bcl transforming protein

Query Match 40.4%; Score 407; DB 2; Length 236;
Best Local Similarity 35.8%; Pred. No. 2.6e-30;
Matches 83; Conservative 34; Mismatches 63; Indels 52; Gaps 3;

QY 9 DTRALVADFVGKLRQKGY----- 27
D 10 DNREIVMKYIHYKLSQRYEWDGDSAPLRAAPTGFISFQESNRTPAVHRDFAART 69
QY 28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRF 81
D 70 SPLRPLVANAGPALSPVPVVLTLFRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
QY 82 VSDELFGQGNWGRGLVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWTHSS 141
D 130 VVEELFRDGVNMGRIVAFVFGVGVNREMSPLVDNIALWMTEYLNRRHLHTWIQDN 189
QY 142 GGWAEFTALYGDGALEEARLRREGNWAASVRLTGAVALGALVTGCAFFASK 193
D 190 GGWDAFVELYG----PSMRPLDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236

RESULT 9
TVMSA1
transforming protein bcl-2-alpha - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C:Accession: A25960; E37332
R:Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A:Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
A:Reference number: A90893; MUID:87187643; PMID:3032455
A:Accession: A25960
A:Molecule type: DNA
A:Residues: 1-236 <NEG>
A:Cross-references: GB:L31532; GB:M16506; NID:G468336; PIDN:AAA37282.1; PID:G387109
R:Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A:Reference number: A37332; MUID:92375724; PMID:1508712
A:Accession: E37332
A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A:Molecule type: DNA
A:Residues: 1-33, 'E', 34-220, 'AL', 223-236 <EGU>
C:Genetics:
A:Gene: BCL2
A:Introns: 192/3
C:Superfamily: bcl transforming protein
C:Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 40.3%; Score 406; DB 1; Length 236;
Best Local Similarity 37.1%; Pred. No. 3.4e-30;
Matches 86; Conservative 33; Mismatches 61; Indels 52; Gaps 5;
```

```
QY 9 DTRALVADFVGKLRQKGYVCGAG-----PG----- 34
D 10 DNREIVMKYIHYKLSQRYEWDGADAAPLGAAPTGFISFQESNPMPAVHREMAART 69
QY 35 -----EGPAADP---LHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRF 81
D 70 SPLRPLVATAGPALSPVPVVLTLFRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
QY 82 VSDELFGQGNWGRGLVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWTHSS 141
D 130 VVEELFRDGVNMGRIVAFVFGVGVNREMSPLVDNIALWMTEYLNRRHLHTWIQDN 189
QY 142 GGWAEFTALYGDGALEEARLRREGNWAASVRLTGAVALGALVTGCAFFASK 193
D 190 GGWDAFVELYG----PSMRPLDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236

RESULT 10
167431
BCL-X-Long - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I67431
R:Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A:Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equi
nstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A:Reference number: I53295; MUID:95129487; PMID:7828536
A:Accession: I67431
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-233 <RES>
A:Cross-references: EMBL:U34963; NID:G1004376; PIDN:AAA77686.1; PID:G1004377
C:Superfamily: bcl transforming protein

Query Match 40.2%; Score 404.5; DB 2; Length 233;
Best Local Similarity 39.6%; Pred. No. 4.7e-30;
Matches 89; Conservative 22; Mismatches 61; Indels 53; Gaps 4;

QY 11 RALVADFVGKLRQKGY-----V 28
D 6 RELVVDFLSYKLSQKYSWSQFSDVENRTEAPEETEPERTPSAINGNPSWHLADSPAV 65
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRF 80
D 66 NGA-TGHSSSIDAREVLPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTVYQSFE 124
QY 81 QVSDELFGQGNWGRGLVAFVFGAALCAESVKNKEMEPLVGQVQEWVAYLETRLADWTHS 140
D 125 QVNELFRDGVNMGRIVASSSFGGALCVESVDKEMQVLVSRIASWMATYLNHDHLEPWIOE 184
QY 141 SGGWAEFTALYGDGALEEARLR--GNWASVRLTGTGAVALGAL 183
D 185 NGGWDTFVDLYGNNTAPESRKQERENRWFLTGMTVAGVVLGSL 229
```

```
RESULT 11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C:Species: Cricetulus griseus (Chinese hamster)
C:Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C:Accession: JC7383
R:Tomicic, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A:Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A:Reference number: JC7383
A:Contents: Ovary
A:Accession: JC7383
A:Molecule type: mRNA
A:Residues: 1-236 <TOM>
A:Cross-references: GB:AJ271720
C:Comment: This protein has anti-apoptotic function, and supports cell survival.
C:Genetics:
```



transforming protein (bcl-2-beta) - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 24-Apr-1998  
C;Accession: B37332; S35452  
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A;Title: Isolation and Characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A;Reference number: A37332; MUID:92375724; PMID:1508712  
A;Accession: B37332  
A;Status: nucleic acid sequence not shown  
A;Molecule type: DNA  
A;Residues: 1-216 <EGU>  
A;Cross-references: EMBL:D11381; EMBL:D11382  
C;Superfamily: bcl transforming protein

Query Match	35.4%	Score 356;	DB 2;	Length 216;
Best Local Similarity	38.4%	Pred.No. 1.3e-25;		
Matches	71;	Conservative	21;	Mismatches 49; Indels 44; Gaps 2;

  

QY	9	DTALVADFVGYKLRQGYVCGAG-----PGECPAADP-----	41
Db	10	DNRETVLKYIHYKLSQRGYDWAAGEORPPVPPAPAPAPAAVAAAGASSHRRPEPGSA	69
QY	42	-----LHQAMRAAGDEFETFRRTFSDLAQLHVTTPGSAQQRFTQVSD	84
Db	70	AASEVPPAEGLRPAPPGVHLALRQAGDEFSSRYQORDFAQMSGQLHTPFTAHGRFVAVVE	129
QY	85	ELFQGGPNWGRLVAFVFGAALCAESYNKEMEPLVQGVQEWVAYLETRLADWTHSSGGW	144
Db	130	ELFRDGVNMGRIVAFEFEGGVNMCVESVNRMSPLVDNIATWNTEYLNRLHLHNWICNGGW	189
QY	145	AEPTA	149
Db	190	VRACA	194

Search completed: October 24, 2003, 10:52:02  
Job time : 27 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:26:35 ; Search time 13.5 Seconds  
(without alignments)  
672.308 Million cell updates/sec

Title: US-09-925-674A-7  
Perfect score: 1007  
Sequence: 1 MATPASAPDTRALVDFVG.....LTGAVALGALVTGCAFFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1007	100.0	193	1 BCLW_HUMAN	Q92843 homo sapien
2	1000	99.3	193	1 BCLW_MOUSE	P70345 mus musculus
3	646.5	64.2	228	1 AR1_XENLA	Q91827 xenopus lae
4	432.5	42.9	229	1 BCLX_CHICK	Q07816 gallus gall
5	431.5	42.9	233	1 BCLX_PIG	C77737 sus scrofa
6	428.5	42.6	233	1 BCLX_HUMAN	Q07817 homo sapien
7	428.5	42.6	233	1 BCLX_MOUSE	Q64373 mus musculus
8	428.5	42.6	233	1 BCLX_RAT	P53563 rattus norv
9	423.5	42.1	233	1 BCL2_CHICK	Q0709 gallus gall
10	416.5	41.4	229	1 BCL2_BOVIN	Q02718 bos taurus
11	414	41.1	236	1 BCL2_RAT	P49950 rattus norv
12	413	41.0	236	1 BCL2_MOUSE	P10417 mus musculus
13	412.5	41.0	239	1 BCL2_HUMAN	P10415 homo sapien
14	403	40.0	236	1 BCL2_CRIO	Q9jjv8 cricetus
15	371	36.8	204	1 AR11_XENLA	Q91828 xenopus lae
16	177.5	17.6	208	1 BAK_MOUSE	Q08734 mus musculus
17	176	17.5	211	1 BAK_HUMAN	Q16611 homo sapien
18	173	17.2	211	1 BAK2_HUMAN	Q13014 homo sapien
19	155.5	15.4	192	1 BAXA_MOUSE	Q07813 mus musculus
20	154.5	15.3	192	1 BAXA_RAT	Q63690 rattus norv
21	153	15.2	192	1 BAXA_HUMAN	Q07812 homo sapien
22	150	14.9	280	1 CED9_CAEEL	P41958 caenorhabdi
23	147	14.6	192	1 BAX3_BOVIN	Q02703 bos taurus
24	146.5	14.5	218	1 BAX3_HUMAN	Q07814 homo sapien
25	143	14.2	177	1 NR13_COTJA	Q90343 coturnix co
26	137.5	13.7	143	1 BAXD_HUMAN	P55269 homo sapien
27	136.5	13.6	271	1 CED9_CAEBR	P41957 caenorhabdi
28	118	11.7	175	1 BFL1_HUMAN	Q16548 homo sapien
29	117	11.6	194	1 BCLB_HUMAN	Q9hd36 homo sapien
30	112	11.1	350	1 MCL1_HUMAN	Q07820 homo sapien
31	105	10.4	172	1 BFL1_MOUSE	Q07440 mus musculus
32	99.5	9.9	179	1 EAR_ASFM2	Q07819 african swi
33	98.5	9.8	179	1 EAR_ASFB7	P42485 african swi

RESULT 1				
BCLW_HUMAN				
ID	BCLW_HUMAN	STANDARD;	PRT;	193 AA.
AC	Q92843;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Apoptosis regulator Bcl-w (BCL2-like 2 protein).			
GN	BCL2L2 OR BCLW OR KIAA0271.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominini			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=96358615; PubMed=8761287;			
RA	Gibson L., Holmgreen S.P., Huang D.C., Bernard O			
RA	Jenkins N.A., Sutherland G.R., Baker E., Adams J			
RT	"bcl-w, a novel member of the bcl-2 family, prom			
RL	Oncogene 13:665-675(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97191544; PubMed=9039502;			
RA	Nagase T., Seki N., Ishikawa K.-I., Ohira M., Ka			
RA	Ohara O., Tanaka A., Kotani H., Miyajima N., Nom			
RT	"Prediction of the coding sequences of unidentifi			
RT	The coding sequences of 80 new genes (K1AA0201-K			
RT	analysis of cDNA clones from cell line KG-1 and			
RL	DNA Res. 3:321-329(1996).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lung;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Der			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen			
RA	Autschui S.F., Zeeberg B., Buetow K.H., Schaefer			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wan			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casava			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carni			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramo			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J			
RA	Richards S., Worley K.C., Hale S., Garcia A.M.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X			
RA	Fahey J., Helton E., Kettman M., Madan A., Rod			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dick			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R			
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U,			
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M			
RT	"Generation and initial analysis of more than 15			
RT	human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(200			
CC	-!- FUNCTION: PROMOTES CELL SURVIVAL.			
CC	-!- SUBCELLULAR LOCATION: Cytoplasmic.			

ALIGNMENTS

34	98.5	9.8	179	1	EAR_ASFE4	Q07818 african swi
35	87	8.6	3433	1	POLG_KUNJM	P14335 k genome pc
36	85.5	8.5	358	1	GLNA_LACSA	P23712 lactuca sat
37	85	8.4	275	1	DAPB_AGR75	Q8uiv8 agrobacteri
38	83.5	8.3	660	1	SOHC_BRAJA	P54924 bradyrhizob
39	82.5	8.2	1440	1	POLG_JAEVN	P14403 j genome po
40	82.5	8.2	3432	1	POLG_JAEVJ	P32886 j genome po
41	90	7.9	541	1	FTCD_MOUSE	Q9ixd4 m formimido
42	79.5	7.9	872	1	SYA_STRPN	Q97q48 streptococc
43	79	7.8	396	1	PORA_PYRFU	Q51804 pyrococcus
44	79	7.8	541	1	FTCD_RAT	O88618 r formimido
45	79	7.8	3430	1	POLG_WNV	P06935 w genome po



CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
CC AND SALIVARY GLAND.  
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
CC FUNCTION.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC  
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CC  
CC -----  
CC EMBL; U59747; AAB09055.1; -.  
CC EMBL; D87461; BAA19666.1; -.  
CC EMBL; BC021198; AAH21198.1; -.  
CC HSSP; Q07817; 1MAZ.  
CC Genew; HGNC:995; BCL2L2.  
CC MIM; 601931; -.  
CC GO; GO:0008189; F:apoptosis inhibitor activity; TAS.  
CC GO; GO:0006916; P:anti-apoptosis; TAS.  
CC GO; GO:0007283; P:spermatogenesis; TAS.  
CC InterPro; IPRC00712; Bcl2\_BH.  
CC InterPro; IPR003093; Bcl2\_BH4.  
CC InterPro; IPR002475; BCL2\_family.  
CC Pfam; PF00452; Bcl-2; 1.  
CC Pfam; PF02180; BH4; 1.  
CC SMART; SM00337; BCL; 1.  
CC SMART; SM00265; BH4; 1.  
CC PROSITE; PS50062; BCL2\_FAMILY; 1.  
CC PROSITE; PS01080; BH1; 1.  
CC PROSITE; PS01258; BH2; 1.  
CC PROSITE; PS01260; BH4\_1; 1.  
CC PROSITE; PS50063; BH4\_2; 1.  
KW Apoptosis.  
FT DOMAIN 9 29 BH4.  
FT DOMAIN 85 104 BH1.  
FT DOMAIN 136 151 BH2.  
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;  
  
Query Match 100.0%; Score 1007; DB 1; Length 193;  
Best Local Similarity 100.0%; Pred. No. 1.9e-83;  
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db |||||  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db |||||  
QY 61 FSDLAALHVTGPSAQORFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
Db |||||  
QY 61 FSDLAALHVTGPSAQORFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
Db |||||  
QY 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
Db |||||  
QY 121 QVQEWVMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
Db |||||  
QY 181 GALVTVGAFVASK 193  
Db |||||  
QY 181 GALVTVGAFVASK 193  
Db |||||  
  
RESULT 2  
BCLW\_MOUSE STANDARD; PRT; 193 AA.  
ID BCLW\_MOUSE  
AC P70345;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Apoptosis regulator Bcl-w (BCL2-like 2 protein).  
GN BCL2L2 OR BCLW.  
CS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
CX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358615; PubMed=8761287;  
RA Gibson L., Holmgren S.P., Huang D.C., Bernard O., Copeland N.G.,  
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;  
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
RL Oncogene 13:665-675(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=C57BL/10J;  
RX MEDLINE=98160183; PubMed=9500547;  
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,  
RA Russell L.D., Macgregor G.R.;  
RT "Testicular degeneration in Bclw-deficient mice.";  
RL Nat. Genet. 18:251-256(1998).  
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
CC AND SALIVARY GLAND.  
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
CC FUNCTION.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC  
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CC  
CC -----  
CC EMBL; U59746; AAB09056.1; -.  
CC EMBL; AF030769; AAB86430.1; -.  
CC HSSP; Q07817; 1MAZ.  
CC MGD; MGI:108052; Bcl2l2.  
CC InterPro; IPR000712; Bcl2\_BH.  
CC InterPro; IPR003093; Bcl2\_BH4.  
CC InterPro; IPR002475; BCL2\_family.  
CC Pfam; PF00452; Bcl-2; 1.  
CC Pfam; PF02180; BH4; 1.  
CC SMART; SM00337; BCL; 1.  
CC SMART; SM00265; BH4; 1.  
CC PROSITE; PS50062; BCL2\_FAMILY; 1.  
CC PROSITE; PS01080; BH1; 1.  
CC PROSITE; PS01258; BH2; 1.  
CC PROSITE; PS01260; BH4\_1; 1.  
CC PROSITE; PS50063; BH4\_2; 1.  
KW Apoptosis.  
FT DOMAIN 9 29 BH4.  
FT DOMAIN 85 104 BH1.  
FT DOMAIN 136 151 BH2.  
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;  
  
Query Match 99.3%; Score 1000; DB 1; Length 193;  
Best Local Similarity 99.0%; Pred. No. 7.6e-83;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db |||||  
QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db |||||  
QY 61 FSDLAALHVTGPSAQORFTQVSDDELFGQGNWGRLLVAFVFGAALCAESVNKEMEPLVG 120  
Db |||||  
  
Query Match 99.3%; Score 1000; DB 1; Length 193;  
Best Local Similarity 99.0%; Pred. No. 7.6e-83;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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DB 61 FSLAAQJHVTPGSAQQRTQVSDLEFQGGPNWGRVLAFFVFGAALCAESVKNKEMEPLVG 120
QY 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRVTLTGAVAL 180
DB 121 QVQEMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRVTLTGAVAL 180
QY 181 GALVTVGAFASK 193
DB 181 GALVTVGAFASK 193

RESULT 3
AR1_XENLA
ID AR1_XENLA STANDARD; PRT; 228 AA.
AC Q91827;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator R1 (XR1) (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head;
RX MEDLINE=95331613; PubMed=7607538;
RA Cruz-Reyes J., Tata J.R.;
RT "Cloning, characterization and expression of two Xenopus bcl-2-like
RT cell-survival genes.";
RL Gene 158:171-179(1995).
CC -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL; X82462; CAA57845.1; -
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_family.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SMC0337; BCL; 1.
DR SMART; SMC0265; BH4; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS50062; BCL2_FAMILY; 1.
KW Apoptosis; Transmembrane.
FT NON_TER 1
FT DOMAIN 120 139 BH1.
FT DOMAIN 171 186 BH2.
FT TRANSMEM 207 227 POTENTIAL.
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 64.2%; Score 646.5; DB 1; Length 228;
Best Local Similarity 67.9%; Pred. No. 5e-51;
Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;

QY 10 TRALVADFVGKLRQKGYVCGAGPGEGPAADPJHQAMRAAGDEFETRFRRTFSDLAQLH 69
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DB 48 SRALVEDLVRYKLCQRSLV--PEPSGAASCALHSAMRAAGDEFEEFRQAFSESTQIH 104
QY 70 VTPGSAQQRTQVSDLEFQGGPNWGRVLAFFVFGAALCAESVKNKEMEPLVGQVQEMWVAY 229
DB 105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVKNKEMSPLLPRICQWMTY 164
QY 130 LETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRVTLTGAVALGALVTVGAF 189
DB 165 LETNLRDWIQSNGGNGFLTYGDGAIEEARRQREGNWSLKTVLTGAVALGALMTVGAL 224
QY 190 FASK 193
DB 225 FASK 228

RESULT 4
BCLX_CHICK
ID BCLX_CHICK STANDARD; PRT; 229 AA.
AC Q07816; Q98908;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).
GN BCL2L1 OR BCLX OR BCL-X.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RX MEDLINE=93364977; PubMed=8358789;
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT of apoptotic cell death.";
RL Cell 74:597-608(1993).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM LONG).
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;
RX MEDLINE=97264485; PubMed=9110311;
RA Vilagrasa X., Mezquita C., Mezquita J.;
RT "Differential expression of bcl-2 and bcl-x during chicken
RT spermatogenesis.";
RL Mol. Reprod. Dev. 47:26-29(1997).
CC -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT
CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR
CC ENVELOPE (BY SIMILARITY).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q07816-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q07816-2; Sequence=VSP_000514;
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID
CC DEVELOPMENT.
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC
CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-
CC APOPTOTIC ACTIVITY (BY SIMILARITY).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL; Z23110; CAA080657.1; -.
DR EMBL; U26645; AAB07677.1; -.
DR PIR; A47537; A47537.
DR HSSP; P53563; IAF3.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_FAMILY.
DR InterPro; IPR004725; Bcl2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00063; BH4_2; 1.
KW Apoptosis; Transmembrane; Alternative splicing.
FT DOMAIN 4 24 BH4.
FT DOMAIN 82 96 BH3.
FT DOMAIN 125 144 BH1.
FT DOMAIN 176 191 BH2.
FT TRANSMEM 206 223 POTENTIAL.
FT VARSELIC 185 229 ERFVDLYGNNAAEELRKQGETFNKWLTCATVAGVLLGLGSJ
FT LSRK -> VRTALP (in isoform Short).
FT /FTID=VSP_C00514.
SQ SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;

Query Match 42.9%; Score 432.5; DB 1; Length 229;
Best Local Similarity 41.7%; Pred. No. 8.3e-32;
Matches 95; Conservative 22; Mismatches 62; Indels 49; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----VCGAGPGEGP----- 37
Db 6 RELVIDFVSYKLSQRGHWCSEEEEDENRTDTAAEAEMDSVLNGSPSWHPPAGHVNGAT 65

QY 38 -----AADPLHQAMRAAGDEFETFRFRRTFSDLAALQJHVTGPSAQQRFTQVSDS 85
Db 66 VHRSSLEVHEIVRASDVROALRDAGDEFELRYRRAPFSDLTSQLHIITPGTAYQSFEQVVNE 125

QY 86 LFQGGPNWGRVAFVFGAALCAESVNKEMEPVLGVQVQEMVAYLETRLADWIHSSGGWA 145
Db 126 LFHDGVNWGRIVAFSFGGALCVESVDKEMRVLVGRIVSWMTTYLTDLDPWIOENGWGE 185

QY 146 EFTALYGDGALEEARLRREGNWASVRTVLTGAVAGALVTVGAFASK 193
Db 186 RFVDLYGNNA---AAELRKQGETFNKWLTCATVAGVLL-LGSLLSRK 229

RESULT 5
BCLX_PIG STANDARD; PRT; 233 AA.
AC 077737;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).
GN BCL2L1 OR BCL2L OR BCLX.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99171363; PubMed=10072723;
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;
RT "Quantification of cardioprotective gene expression in porcine
RT short-term hibernating myocardium.";
```

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RL J. Mol. Cell. Cardiol. 31:147-158(1999).
CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-
CC apoptotic activity is inhibited by association with SIVA isoform
CC 1. Inhibits activation of caspases (By similarity). Appears to
CC regulate cell death by blocking the voltage-dependent anion
CC channel (VDAC) by binding to it and preventing the release of the
CC caspase activator, cytochrome c, from the mitochondrial membrane.
CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC similarity). Heterodimerization with BAX does not seem to be
CC required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC x(L) binds to Siva isoform 1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC envelope (By similarity).
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC The BH1 and BH2 domains are required for both heterodimerization
CC with other Bcl2 family members and for repression of cell death.
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis (By
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC apoptotic activity (By similarity).
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
DR EMBL; AJ001203; CAA04597.1; -.
DR HSSP; Q07817; IMAZ.
DR InterPro; IPR000712; Bcl2_BH.
DR InterPro; IPR003093; Bcl2_BH4.
DR InterPro; IPR002475; BCL2_FAMILY.
DR InterPro; IPR004725; BCL2_reg.
DR Pfam; PF00452; Bcl-2; 1.
DR Pfam; PF02180; BH4; 1.
DR SMART; SM00337; BCL; 1.
DR SMART; SM00265; BH4; 1.
DR TIGRFAMs; TIGR00865; bcl-2; 1.
DR PROSITE; PS00062; BCL2_FAMILY; 1.
DR PROSITE; PS01080; BH1; 1.
DR PROSITE; PS01258; BH2; 1.
DR PROSITE; PS01259; BH3; 1.
DR PROSITE; PS01260; BH4; 1.
DR PROSITE; PS00063; BH4_2; 1.
KW Apoptosis; Mitochondrion; Transmembrane.
FT DOMAIN 4 24 BH4.
FT DOMAIN 86 100 BH3.
FT DOMAIN 129 148 BH1.
FT DOMAIN 180 195 BH2.
FT TRANSMEM 210 226 POTENTIAL.
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA0441912B2 CRC64;

Query Match 42.9%; Score 431.5; DB 1; Length 233;
Best Local Similarity 41.8%; Pred. No. 1e-31;
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28
Db 6 RELVDFLSYKLSQKGSWSQFTDVEENRTEAPEGTESEAETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETFRFRRTFSDLAALQJHVTGPSAQQRFT 80
Db 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAPFSDLTSQLHIITPGTAYQSFE 124

QY 81 QVSDELFGGPNWGRVAFVFGAALCAESVNKEMEPVLGVQVQEMVAYLETRLADWIHS 140
Db 125 QVLNELFRDGVNWGRIVAFSFGGALCVESVDKEMQVLVSRIATWMTYLNCHLEPWICE 184
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QY      141 SGGWAEFTALYDGALEEARLR--GNWASVRTVLGTGAVALGAL 193
      :||| | |||: | |||: | |||: | |||: | |||: | |||:
Db      185 NGGWDTFVELYGNNAAESRKQGERFNRWFLTMGLTGMVLGSL 229

RESULT 6
BCLX_HUMAN
ID      BCLX_HUMAN      STANDARD;      PRT;      233 AA.
AC      Q07817; Q92976;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Apoptosis regulator Bcl-x (BCL2-like 1 protein).
GN      BCL2L1 OR BCL2L OR BCLX.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RX      MEDLINE=93364977; PubMed=8358789;
RA      Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,
RA      Turka L.A., Mao X., Nunez G., Thompson C.B.;
RT      "bcl-x, a bcl-2-related gene that functions as a dominant regulator
RT      of apoptotic cell death.";
RL      Cell 74:597-608(1993).
[2]
SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RA      Inohara N., Ohta S.;
RL      Submitted (Oct-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A. (ISOFORM X(L)).
TISSUE=Lung;
RX      MEDLINE=22388257; PubMed=12477932;
RA      Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA      Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA      Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA      Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA      Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA      Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA      Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA      Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA      Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA      Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA      Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA      Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA      Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA      Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA      Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA      Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalius D.E.,
RA      Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT      "Generation and initial analysis of more than 15,000 full-length
RT      human and mouse cDNA sequences.";
RL      Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
MUTAGENESIS OF GLY-138, AND HETERODIMERIZATION.
RX      MEDLINE=95372373; PubMed=7644501;
RA      Sedlak T.W., Oltvai Z.N., Yang E., Wang K., Boise J.H., Thompson C.B.,
RA      Korsmeyer S.J.;
RT      "Multiple Bcl-2 family members demonstrate selective dimerizations
RT      with Bax.";
RL      Proc. Natl. Acad. Sci. U.S.A. 92:7834-7838(1995).
[5]
MUTAGENESIS OF BH1 AND BH2 DOMAINS.
RX      MEDLINE=96170038; PubMed=8596636;
RA      Cheng E.H.-Y., Levine B., Boise L.H., Thompson C.E., Hardwick J.M.,
RA      Korsmeyer S.J.;
RT      "Bax-independent inhibition of apoptosis by Bcl-XL.";
RL      Nature 379:554-556(1996).
[6]
INTERACTION WITH SIVA.
RX      PubMed=12011449;
```

Xue L., Chu F., Cheng Y., Sun X., Borthakur A., Ramarao M., Pandey P., Wu M., Schlossman S.F., Prasad K.V.S.;  
"Siva-1 binds to and inhibits BCL-X(L)-mediated protection against UV radiation-induced apoptosis.";  
Proc. Natl. Acad. Sci. U.S.A. 99:6925-6930(2002).  
[7]  
STRUCTURE BY NMR OF 1-209.  
RX MEDLINE=97172562; PubMed=9020082;  
RA Sattler M., Liang H., Nettlesheim D., Meadows R.P., Harlan J.E.,  
RA Eberstadt M., Yoon H.S., Shuker S.B., Chang B.S., Minn A.J.,  
RA Thompson C.B., Fesik S.W.;  
RT "Structure of Bcl-xL-Bak peptide complex: recognition between  
RT regulators of apoptosis.";  
RL Science 275:983-986(1997).  
[8]  
X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS), AND STRUCTURE BY NMR OF 1-209.  
RX MEDLINE=96256675; PubMed=8692274;  
RA Muchmore S.W., Sattler M., Liang H., Meadows R.P., Harlan J.E.,  
RA Yoon H.S., Nettlesheim D., Chang B.S., Thompson C.B., Wong S.L.,  
RA Ng S.L., Fesik S.W.;  
RT "X-ray and NMR structure of human Bcl-xL, an inhibitor of programmed  
RT cell death.";  
RL Nature 381:335-341(1996).  
[9]  
CLEAVAGE BY CASPASES, AND MUTAGENESIS OF ASP-61.  
RX MEDLINE=98118550; PubMed=9435230;  
RA Clem R.J., Cheng E.H.-Y., Karp C.L., Kirsch D.G., Ueno K.,  
RA Takahashi A., Kastan M.B., Griffin D.E., Earnshaw W.C., Veliuona M.A.,  
RA Hardwick J.M.;  
RT "Modulation of cell death by Bcl-xL through caspase interaction.";  
RL Proc. Natl. Acad. Sci. U.S.A. 95:554-559(1998).  
CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-  
CC apoptotic activity is inhibited by association with SIVA isoform  
CC 1. Inhibits activation of caspases (By similarity). Appears to  
CC regulate cell death by blocking the voltage-dependent anion  
CC channel (VDAC) by binding to it and preventing the release of the  
CC caspase activator, cytochrome c, from the mitochondrial membrane.  
CC The Bcl-x(S) isoform promotes apoptosis.  
CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2.  
CC Heterodimerization with BAX does not seem to be required for anti-  
CC apoptotic activity. Isoform Bcl-x(L) binds to Siva isoform 1.  
CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear  
CC envelope (By similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=3;  
CC Name=Bcl-x(L);  
CC IsoId=Q07817-1; Sequence=Displayed;  
CC Name=Bcl-x(S);  
CC IsoId=Q07817-2; Sequence=VSP\_000515;  
CC Name=Bcl-x(beta);  
CC IsoId=Q07817-3; Sequence=VSP\_000516;  
CC -!- TISSUE SPECIFICITY: Bcl-x(S) is expressed at high levels in cells  
CC that undergo a high rate of turnover, such as developing  
CC lymphocytes. In contrast, Bcl-x(L) is found in tissues containing  
CC long-lived postmitotic cells, such as adult brain.  
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
CC The BH1 and BH2 domains are required for both heterodimerization  
CC with other Bcl2 family members and for repression of cell death.  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
CC activity.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
-----  
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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; 223116; CAA80662.1; -

DR EMBL; 223115; CAA80661.1; -

DR EMBL; U72398; AAB17354.1; -

DR EMBL; BC019307; AAH19307.1; -

DR PIR; B47537; B47537

DR PIR; JE0203; JE0203

DR PDB; 1BXL; 29-OCT-97

DR PDB; 1LXL; 21-APR-97

DR PDB; 1MAZ; 21-APR-97

DR PDB; 1G5J; 07-FEB-01

DR PDB; 1G5M; 21-MAR-01

DR PDB; 1GJH; 13-JUN-01

DR Genew; HGNC:992; BCL2L1.

DR MIM; 600039; -

DR GO; GO:0005739; C:mitochondrion; TAS.

DR GO; GO:0008189; F:apoptosis inhibitor activity; TAS.

DR GO; GO:0006916; P:anti-apoptosis; TAS.

DR GO; GO:0008637; P:apoptotic mitochondrial changes; TAS.

DR GO; GO:0008634; P:negative regulation of survival gene products; TAS.

DR InterPro; IPR000712; Bcl2\_BH.

DR InterPro; IPR003093; Bcl2\_BH4.

DR InterPro; IPR002475; BCL2\_family.

DR InterPro; IPR004725; Bcl2\_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS00662; BCL2\_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4; 1.

DR PROSITE; PS00663; BH4\_2; 1.

KW Apoptosis; Mitochondrion; Alternative splicing; Transmembrane;

KW 3D-structure.

FT DOMAIN 4 24 BH4.

FT DOMAIN 86 100 BH3.

FT DOMAIN 129 148 BH1.

FT DOMAIN 180 195 BH2.

FT TRANSMEM 210 226 POTENTIAL.

FT SITE 62 62 CLEAVAGE (BY CASPASE-1).

FT VARSPLIC 126 188 Missing (in isoform Bcl-X(S)).

FT VARSPLIC 189 233 /FTID=VSP 000515.

FT VARSPLIC 189 233 DTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVLLGSL

FT FSRX -> VRTKPLVCPESLASGQRSPTALLYLFLLCWV

FT VGDVDS (in isoform Bcl-X(beta)).

FT /FTID=VSP 000516.

FT D->A: NO CLEAVAGE BY CASPASE-1 NOR BY

FT CASPASE-3.

FT FRD->VRA: NO HETERODIMERIZATION WITH BAX.

FT VNW->AIL: LOSS OF ANTI-APOPTOTIC

FT ACTIVITY.

FT GRI->ELN: LOSS OF ANTI-APOPTOTIC

FT ACTIVITY.

FT G->A: NO HETERODIMERIZATION WITH BAX.

FT G->E: NO HETERODIMERIZATION WITH BAX.

FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.

FT D->A: NO EFFECT ON CASPASE-1 CLEAVAGE.

FT WD->GA: REDUCES ANTI-APOPTOTIC ACTIVITY

Query Match 42.6%; Score 428.5; DB 1; Length 233;

Best Local Similarity 41.3%; Pred. No. 1.9e-31;

Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28

DB 6 RELVVDFLSYKLSQKYSWSQSDVEENRTEAPEGTESEMETPSAINGNPSMHWADSPAV 65

QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVHTPGSAQORFT 80

Db 66 NGA-TGSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

QY 8i QVSDELFQGGPNWGRVLVAFVFGAALCAESVNKEMEPLVQVQVQVEMVAYLETRLADWIHS 140

Db 125 QVVNELFRDGVNMGRIIVAFFSFGALCVESVDKEMQVLVSRIAAWMAATYLNHLEPWIOE 184

QY 141 SGGWAEFTALYGDGALAEARLRE--GNWASVRTVLTCGAVALGAL 183

Db 185 NGGWDTFVELYGNNAEAESRKQGRFNRWFLTGMTVAGVLLGSL 229

RESULT 7

BCLX\_MOUSE

ID BCLX\_MOUSE STANDARD; PRT; 233 AA.

AC Q64373; Q60657; Q60658; Q61338;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).

GN BCL2L1 OR BCL2L OR BCLX.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2A4B;

RA Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;

RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=95331139; PubMed=7607090;

RA Gonzalez-Garcia M., Perez-Balletero R., Ding L., Duan L., Boise L.H.,

RA Thompson C.B., Nunez G.;

RT "bcl-XL is the major bcl-x mRNA form expressed during murine

RT development and its product localizes to mitochondria.";

RL Development 120:3033-3042(1994).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(DELTA-TM)).

RC TISSUE=Pre-B cell;

RX MEDLINE=95052604; PubMed=7963517;

RA Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;

RT "Cloning and molecular characterization of mouse bcl-x in B and T

RT lymphocytes.";

RL J. Immunol. 153:4388-4398(1994).

RN [4]

RP SEQUENCE FROM N.A. (ISOFORM X(BETA)).

RC STRAIN=C57BL/6 X CBA; TISSUE=Thymus;

RX MEDLINE=98051053; PubMed=9390687;

RA Yang X.-F., Weber G.F., Cantor H.;

RT "A novel Bcl-x isoform connected to the T cell receptor regulates

RT apoptosis in T cells.";

RL Immunity 7:629-639(1997).

RN [5]

RP SEQUENCE FROM N.A.

RX MEDLINE=97289584; PubMed=9144489;

RA Grillo D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,

RA Ohta S., Seldin M.F., Nunez G.;

RT "Genomic organization, promoter region analysis, and chromosome

RT localization of the mouse bcl-x gene.";

RL J. Immunol. 158:4750-4757(1997).

CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-

CC apoptotic activity is inhibited by association with SIVA isoform

CC 1. Inhibits activation of caspases (By similarity). Appears to

CC regulate cell death by blocking the voltage-dependent anion

CC channel (VDAC) by binding to it and preventing the release of the

CC caspase activator, cytochrome c, from the mitochondrial membrane.

CC The Bcl-x(S) isoform promotes apoptosis.

CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By

CC similarity). Heterodimerization with BAX does not seem to be

CC required for anti-apoptotic activity (By similarity). Isoform Bcl-

CC x(L) binds to Siva isoform 1 (By similarity).









CC domains, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).  
CC !- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum (By  
CC similarity).  
CC !- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
CC for interaction with RAF-1 (By similarity).  
CC !- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and  
CC occurs during the G2/M phase of the cell cycle (By similarity). In  
CC the absence of growth factors, Bcl2 appears to be phosphorylated  
CC by other protein kinases such as ERKs and stress-activated  
CC kinases. Dephosphorylated by protein phosphatase 2A (PP2A) (By  
CC similarity).  
CC !- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol  
CC promoting further caspase activity (By similarity).  
CC !- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC !- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC !- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC !- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC !- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U92434; AAB53319.1; --  
CC HSSP; Q07817; IMAZ.  
CC InterPro; IPR000712; Bcl2\_BH.  
CC InterPro; IPR003093; Bcl2\_BH4.  
CC InterPro; IPR002475; BCL2\_family.  
CC InterPro; IPR004725; Bcl2\_reg.  
CC Pfam; PF00452; Bcl-2; 1.  
CC Pfam; PF02180; BH4; 1.  
CC SMART; SMC0337; BCL; 1.  
CC SMART; SMC0265; BH4; 1.  
CC TIGRFAMs; TIGR00865; bcl-2; 1.  
CC PROSITE; PS00062; BCL2\_FAMILY; 1.  
CC PROSITE; PS01080; BH1; 1.  
CC PROSITE; PS01258; BH2; 1.  
CC PROSITE; PS01259; BH3; 1.  
CC PROSITE; PS01260; BH4; 1; 1.  
CC PROSITE; PS50063; BH4\_2; 1.  
CC Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
FT DOMAIN 10 30 BH4.  
FT DOMAIN 64 68 POLY-PRO.  
FT DOMAIN 69 72 POLY-ALA.  
FT DOMAIN 83 97 BH3.  
FT DOMAIN 126 145 BH1.  
FT DOMAIN 177 192 BH2.  
FT TRANSMEM 202 223 POTENTIAL.  
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
FT MOD RES 63 63 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
SQ SEQUENCE 229 AA; 25099 MW; AD1DD0AF98FF1D CRC64;  
  
Query Match 41.4%; Score 416.5; DB 1; Length 229;  
Best Local Similarity 38.2%; Pred. No. 2.3e-30;  
Matches 86; Conservative 35; Mismatches 59; Indels 45; Gaps 5;  
  
QY 9 DTRALVDFVGYKLRQKGYVCGAG-----PGE----- 35  
DB 10 DNREIVMKYIHYKLSQRYEWADGAGAPGAAPAGPILSSQPGRTAPSRTPPPPA 69  
QY 36 ---GPAADP---LHQAMRAAGDEFETFRRTFSDLAQLHVTGSAQQRTQVSDLELQ 88  
DB 70 AAAGPAPSPVPPVWHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPTTARERFATVVEELFR 129

QY 89 GGNWGRLVAFVFGAALCAESVNKEMPLVGQVQEMVAYLETRLADWIHSSGGWAEFT 148  
DB 130 DGVNWGRIVAFVFGGVMCMVESVNREMSPLVDSIALMWTVELNRHLHTWIQDNGSGWDAFV 189  
QY 149 ALYGDGGALEZARRLREGNWASVRTVLTCGAVLGAVALGALVTVGAFFASK 193  
DB 190 ELYG---PSMRPLDFSWLSLKALLSLAL-VGACITLGAYLGHK 229  
  
RESULT 11  
BCL2\_RAT  
ID BCL2\_RAT STANDARD; PRT; 236 AA.  
AC P49950; Q62837; Q64032;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2 OR BCL-2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX XEDLINE=94193015; PubMed=8144041;  
RA Sato T., Irie S., Krajewski S., Reed J.C.;  
RT "Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.";  
RL Gene 140:291-292(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Ovary;  
RX XEDLINE=95129487; PubMed=7828536;  
RA Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;  
RT "Expression of members of the bcl-2 gene family in the immature rat  
RT ovary: equine chorionic gonadotropin-mediated inhibition of granulosa  
RT cell apoptosis is associated with decreased bax and constitutive  
RT bcl-2 and bcl-xlong messenger ribonucleic acid levels.";  
RL Endocrinology 136:232-241(1995).  
RN [3]  
RP SEQUENCE OF 19-172 FROM N.A.  
RX MEDLINE=95059917; PubMed=7969891;  
RA Castren E., Chga Y., Berzaghi M.P., Tzimogiorgis G., Thoenen H.,  
RA Lindholm D.;  
RT "bcl-2 messenger RNA is localized in neurons of the developing and  
RT adult rat brain.";  
RL Neuroscience 61:165-177(1994).  
CC !- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (APAF-1).  
CC !- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and  
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
CC domains, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).  
CC !- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC !- TISSUE SPECIFICITY: Expressed in a variety of tissues, with  
CC highest levels in reproductive tissues. In the adult brain,  
CC expression is localized in mitral cells of the olfactory bulb,  
CC granule and pyramidal neurons of hippocampus, pontine nuclei,  
CC cerebellar granule neurons, and in ependymal cells. In prenatal  
CC brain, expression is higher and localized in the neuroepithelium  
CC and in the cortical plate.  
CC !- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
CC for interaction with RAF-1 (By similarity).  
CC !- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and



occurs during the G2/M phase of the cell cycle. In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases.

Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).

PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity (By similarity).

SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.

SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.

SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.

SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

SIMILARITY: BELONGS TO THE BCL-2 FAMILY.

-----

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EMBL; L14680; AAA53662.1; ..

EMBL; U34964; AAA77687.1; ..

EMBL; S74122; -; NOT\_ANNOTATED\_CDS.

PIR; I53744; I53744.

PIR; I67432; I67432.

HSSP; Q07817; IMAZ.

InterPro; IPR000712; Bcl2\_BH.

InterPro; IPR003093; Bcl2\_BH4.

InterPro; IPR002475; BCL2\_family.

InterPro; IPR004725; Bcl2\_reg.

Pfam; PF00452; Bcl-2; 1.

Pfam; PF02180; BH4; 1.

SMART; SM00337; BCL; 1.

SMART; SM00265; BH4; 1.

TIGRFAMs; TIGR00865; bcl-2; 1.

PROSITE; PS50062; BCL2\_FAMILY; 1.

PROSITE; PS01080; BH1; 1.

PROSITE; PS01258; BH2; 1.

PROSITE; PS01259; BH3; 1.

PROSITE; PS01260; BH4; 1; 1.

PROSITE; PS50063; BH4\_2; 1.

Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.

DOMAIN 10 30 BH4.

DOMAIN 90 104 BH3.

DOMAIN 133 152 BH1.

DOMAIN 184 199 BH2.

TRANSMEM 209 230 POTENTIAL.

SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).

MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).

CONFLICT 42 42 A -> R (IN REF. 2).

CONFLICT 157 157 E -> G (IN REF. 1).

CONFLICT 164 164 S -> Y (IN REF. 2).

CONFLICT 212 212 L -> Q (IN REF. 2).

SEQUENCE 236 AA; 26622 MW; E7688CB9C71A872A CRC64;

Query Match 41.1%; Score 414; DB 1; Length 236;

Best Local Similarity 36.2%; Pred. No. 3.9e-30;

Matches 84; Conservative 34; Mismatches 62; Indels 52; Gaps 3;

-----

9 DTRALVADFVGYKLRQGY----- 27

10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPJRAAFTPGIFSQPESNRTFAVHRDTAART 69

28 -----VCGAGPGEGPADPLHQAMRAAGDEFETFRRTFSDLAAQLHVTTPGSAQQRFTC 81

70 SPLRPLVANAGPALSPVPVVLTLRRAGDDFSRYRDRFAEMSSQLHLTPFTARGFAT 129

82 VSDELFGQGNWGRVLVAFVFGAALCAESVNKEVEPLVGQVQVEMVAYLETRLADWIHSS 141

130 VVEELPRDGVNWGRIVAFEFEGGVMCVESVNREMSPLVDNIALWMTYELNRLHHTWIQDN 189

QY 142 GGWAEFTALYGDGALAEARRLRREGNWNASVRTVLTGAVALGALVTVCAGFAFFASK 193

DB 190 GGWDAFVELYG---PSMRPLDFSWLSIKTLTSLAL-VGACITLGAYLGHK 236

RESULT 12

BCL2\_MOUSE

ID BCL2\_MOUSE STANDARD; PRT; 236 AA.

AC P10417; P10418;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-APR-1993 (Rel. 25, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Apoptosis regulator Bcl-2.

GN BCL2 OR BCL-2.

OS Mus musculus (Mouse).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

CC NCBI\_TaxID=10090;

RN [1];

RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).

RC STRAIN=BALB/c; TISSUE=Liver;

RX MEDLINE=87187643; PubMed=3032455;

RA Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;

RT "Molecular analysis of mbcl-2: structure and expression of the murine gene homologous to the human gene involved in follicular lymphoma.";

RJ Cell 49:455-463(1987).

RN [2];

RP REVISIONS TO 221-222.

RX MEDLINE=92375724; PubMed=1508712;

RA Eguchi Y., Ewert D.L., Tsujimoto Y.;

RT "Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues including lymphoid and neuronal organs in adult and embryo.";

RT Nucleic Acids Res. 20:4187-4192(1992).

RN [3];

RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.

RX MEDLINE=97277291; PubMed=9115213;

RA Ito T., Deng X., Carr B., May W.S. Jr.;

RT "Bcl-2 phosphorylation required for anti-apoptosis function.";

RJ J. Biol. Chem. 272:11671-11673(1997).

RN [4];

RP DEPHOSPHORYLATION BY PP2A.

RX MEDLINE=99069407; PubMed=9852076;

RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;

RT "Reversible phosphorylation of Bcl2 following interleukin 3 or bryostatins 1 is mediated by direct interaction with protein phosphatase 2A\*.";

RJ J. Biol. Chem. 273:34157-34163(1998).

CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1).

CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1.

CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Alpha;

CC IsoId=P10417-1; Sequence=Displayed;

CC Name=Beta;

CC IsoId=P10417-2; Sequence=VSP\_000513;

CC TISSUE SPECIFICITY: Expressed in a variety of tissues.

CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1.

CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and







QY 36 -----GPAADP----LHQAYRAAGDEFEFETFRRTFSDLAALQHLVTPGSAQCR 78  
Db 70 SPLQTPAAGAAAGPALSPVPPVHJTLRQAGDDFSRRYRRDFAEISSQLHLTPFTARGR 129  
QY 79 FTQVSDLEFQGGNMGRLVAFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWI 138  
Db 130 FATVVEELFRDGVNMGRIVAFVFGGVMCVESVNREMSPLVDNIALMTEYLNRLHTWI 189  
QY 139 HSSGGWAEFTALYGDGALBEEARRLRREGNWSVRTVLTGAVALGALVTVGAFPAASK 193  
Db 190 QDNGGWDAFVELYG----PSMRPLDFDSWLSLKLTLALLAL-VGACITLGLAYLGHK 239

RESULT 14  
BCL2-CRIL0  
ID BCL2 CRIL0 STANDARD; PRT; 236 AA.  
AC Q9JUV8;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2.  
OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RX MEDLINE=20431763; PubMed=10973819;  
RA Tomicic M.T., Christmann M., Kaina B.;  
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein."  
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).  
RN [2]  
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.  
RX MEDLINE=21092839; PubMed=11181062;  
RA Tomicic M.T., Kaina B.;  
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9 and caspase-3."  
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).  
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems including factor-dependent lymphohematopoietic and neural cells. Regulates cell death by controlling the mitochondrial membrane permeability. Appears to function in a feedback loop system with caspases. Inhibits caspase activity either by preventing the release of cytochrome c from the mitochondria and/or by binding to the apoptosis-activating factor (APAF-1) (By similarity).  
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2 domains, and is necessary for anti-apoptotic activity (By similarity). Also interacts with APAF-1 and RAF-1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and for interaction with RAF-1 (By similarity).  
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2 anti-apoptotic activity. Growth factor-stimulated phosphorylation on Ser-70 by PKC is required for the anti-apoptosis activity and occurs during the G2/M phase of the cell cycle (By similarity). In the absence of growth factors, Bcl2 appears to be phosphorylated by other protein kinases such as ERKs and stress-activated kinases (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The cleaved protein, lacking the BH4 domain, has pro-apoptotic activity, causes the release of cytochrome c into the cytosol promoting further caspase activity.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.

CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
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CC -----  
CC EMBL; AJ271720; CAB92245.1; -.  
CC PIR; JC7383; JC7383.  
CC HSSP; Q07817; IMAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMS; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
FT DOMAIN 10 30 BH4.  
FT DOMAIN 90 104 BH3.  
FT DOMAIN 133 152 BH1.  
FT DOMAIN 184 199 BH2.  
FT TRANSMEM 209 230 POTENTIAL.  
FT SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).  
FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
SQ SEQUENCE 236 AA; 26491 MW; BECADFIEF3337228 CRC64;  
  
Query Match: 40.0%; Score 403; DB 1; Length 236;  
Best Local Similarity 35.3%; Pred. NO. 3.8e-29;  
Matches 92; Conservative 34; Mismatches 64; Indels 52; Gaps 3;  
  
QY 9 DTRALVADFVGYKLRQKGY----- 27  
Db 10 DNREIVMKYHYKLSQRYEWDVGDVDAALGAAPTGFISFQPSNPTPAVHRDMAART 69  
QY 28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQCRFTQ 81  
Db 70 SPLRPVATTGTLSPVPPVHJTLRQAGDDFSRRYRRDFAEISSQLHLTPFTARGRAFAT 129  
QY 82 VSDELFQGGNMGRLVAFVFGAALCAESVNKEMEPLVGQVQEWVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNMGRIVAFVFGGVMCVESVNREMSPLVDNIALMTEYLNRLHTWIQDN 189  
QY 142 GGWAEFTALYGDGALBEEARRLRREGNWSVRTVLTGAVALGALVTVGAFPAASK 193  
Db 190 GGWDAFVELYG----PSVRPLDFDSWLSLKLTLALLAL-VGACITLGLAYLGHK 236  
  
RESULT 15  
AR11\_XENLA  
ID AR11\_XENLA STANDARD; PRT; 204 AA.  
AC Q91828;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator R11 (XR11).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]

[illegible]

Search completed: October 24, 2003, 10:46:47  
Job time : 15.5 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:43:10 ; Search time 62 Seconds  
(without alignments)  
803.293 Million cell updates/sec

Title: US-09-925-674A-7  
Perfect score: 1007  
Sequence: 1 MATPASAPDTRALVADFVG.....LTGAVALGALVTGGAFFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_23.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriap.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	996	98.9	193	11	O88996
2	956	94.9	193	11	O8CGL4
3	761	75.6	178	11	Q9CYW5
4	761	75.6	178	11	O8CFR2
5	440.5	43.7	233	6	Q9MYW4
6	435.5	43.2	233	11	O35844
7	433.5	43.0	233	6	Q8SQ42
8	431.5	42.9	233	6	Q9N1A2
9	428.5	42.6	233	6	Q9MZS7
10	413	41.0	236	11	O8BQK4
11	403	40.0	238	13	Q90Z98
12	401	39.8	180	6	Q9BDJ5
13	401	39.8	217	11	Q99N35
14	399	39.6	236	11	Q923R6
15	398.5	39.6	180	6	Q9BDX7
16	396.5	39.4	235	6	Q8I008

17	374.5	37.2	188	11	Q9QWX2	Q9gwx2 mus musculu
18	374.5	37.2	235	11	O35843	O35843 mus musculu
19	373.5	37.1	188	4	Q9H1R6	Q9h1r6 homo sapien
20	373	37.0	204	13	Q90ZH2	Q90zh2 xenopus lae
21	354	35.2	185	6	Q8MJ81	Q8mj81 bos taurus
22	347	34.5	219	11	Q99N36	Q99n36 mus musculu
23	343.5	34.1	199	11	Q8C5P0	Q8c5p0 mus musculu
24	296	29.4	89	13	Q8UWJ1	Q8uwj1 gallus gall
25	189	18.8	209	11	Q9JK59	Q9jk59 rattus norv
26	185	18.4	170	11	Q9WJ15	Q9wui5 rattus norv
27	184	18.3	209	11	Q8C264	Q8c264 mus musculu
28	176.5	17.5	192	13	Q919N4	Q919n4 brachydario
29	175.5	17.4	190	4	Q8NFF3	Q8nff3 homo sapien
30	171.5	17.0	221	13	Q98U13	Q98ui3 xenopus lae
31	168.5	16.7	125	4	Q9H1R5	Q9h1r5 homo sapien
32	163	16.2	58	11	Q9R1B3	Q9r1b3 rattus norv
33	162	16.1	235	5	Q967D2	Q967d2 geodia cydo
34	159.5	15.8	163	6	Q9WZS6	Q9mzs6 ovis aries
35	155.5	15.4	173	11	Q8K3J2	Q8k3j2 mus musculu
36	153	15.2	173	4	Q8WZ49	Q8wz49 homo sapien
37	153	15.2	173	11	Q9JKL3	Q9jkl3 rattus norv
38	152	15.1	67	6	Q8MJB3	Q8mjb3 cervus elap
39	148.5	14.7	218	5	Q9N754	Q9n754 suberites d
40	148	14.7	192	6	Q8SQ43	Q8sq43 felis silve
41	147	14.6	192	6	Q8HYU5	Q8hyu5 canis fami1
42	146.5	14.5	179	4	Q9NYG7	Q9nyg7 homo sapien
43	144	14.3	149	6	Q9GMG7	Q9gmg7 ovis aries
44	143	14.2	177	13	Q90ZN1	Q90zn1 gallus gall
45	142.5	14.2	179	12	Q9E1F2	Q9elf2 meleagrid h

ALIGNMENTS

RESULT 1

C88996	ID	O88996	PRELIMINARY;	PRT;	193 AA.
AC	O88996;				
DT	01-NOV-1998	(TRENBLrel. 08, Created)			
DT	01-NOV-1998	(TRENBLrel. 08, Last sequence update)			
DT	01-JUN-2002	(TRENBLrel. 21, Last annotation update)			
DE	Bcl-w.				
GN	BCL-W.				
OC	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;				
RX	MEDLINE=99292146; PubMed=10366024;				
RA	Hamner S., Skoglosa Y., Lindholm D.;				
RT	"Differential expression of bcl-w and bcl-x messenger RNA in the				
RT	developing and adult rat nervous system."				
RL	Neuroscience 91:673-684(1999).				
DR	EMBL; AF096291; AAC64200.1; -.				
DR	HSSP; Q07817; IMAZ.				
DR	InterPro; IPR000712; Bcl2_BH.				
DR	InterPro; IPR003093; Bcl2_BH4.				
DR	InterPro; IPR002475; BCL2_family.				
DR	Pfam; PF00452; Bcl-2; 1.				
DR	Pfam; PF02180; BH4; 1.				
DR	SMART; SM00337; BCL; 1.				
DR	SMART; SM00265; BH4; 1.				
DR	PROSITE; PS50062; BCL2_FAMILY; 1.				
DR	PROSITE; PS01080; BH1; 1.				
DR	PROSITE; PS01258; BH2; 1.				
DR	PROSITE; PS01260; BH4_1; 1.				
DR	PROSITE; PS50063; BH4_2; 1.				
SQ	SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;				

Query Match 98.9%; Score 996; DB 11; Length 193;  
Best Local Similarity 98.4%; Pred. No. 2.9e-81;



Matches 190; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
|||||  
Db 1 MATPASTPTDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
|||||

QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDSELFQGGPNWGRJLVAFVFGAALCAESVNKEMEPLVG 120  
|||||  
Db 61 FSDLAAQLHVTTPGSAQQRFTQVSDSELFQGGPNWGRJLVAFVFGAALCAESVNKEMEPLVG 120  
|||||

QY 121 QVQEWMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
|||||  
Db 121 QVQDMMVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
|||||

QY 181 GALVTVGAFPAASK 193  
|||||  
Db 181 GALVTVGAFPAASK 193  
|||||

RESULT 2  
Q8CGL4 PRELIMINARY; PRT; 193 AA.

AC Q8CGL4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Bcl2-like protein 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Skin;  
RA Su H.-Y.;  
RT "Extraction from neonatal mouse skin after IGF-1 stimulation."  
RL Submitted (OCT-2002) to the EMBL/GenBank/DCBJ databases.  
DR EMBL; AY170344; AAC13177.1; -.  
SQ SEQUENCE 193 AA; 20950 MW; 258AC1818166DFAC CRC64;

Query Match 94.9%; Score 956; DB 1; Length 193;  
Best Local Similarity 95.3%; Pred. No. 1.1e-77;  
Matches 184; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
|||||  
Db 1 MATPASTPTDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDELQTRFRRT 60  
|||||

QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDSELFQGGPNWGRJLVAFVFGAALCAESVNKEMEPLVG 120  
|||||  
Db 61 FSHLAAQLHVTTPGSAQQRFTQVSDSELFQGGPNWGRJLVAFVFGAALCAESVNKEMEPLVG 120  
|||||

QY 121 QVQEWMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
|||||  
Db 121 QVQDMMVAYLETRLAYWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
|||||

QY 181 GALVTVGAFPAASK 193  
|||||  
Db 181 GALVTVGAFPAASK 193  
|||||

RESULT 3  
Q9CYW5 PRELIMINARY; PRT; 178 AA.

ID Q9CYW5  
AC Q9CYW5;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Bcl2-like 2.  
GN BCL2L2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI\_TaxID=10090;  
[1]  
SEQUENCE FROM N.A.  
STRAIN=C57BL/6J; TISSUE=Embryo;  
MEDLINE=21085660; PubMed=11217851;  
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Fieischmann W., Gaasterland T., Glissi C., King B., Kochiwa H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
Schröml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momabaerts P.,  
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,  
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohetsuki S.,  
Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK013244; BAB28740.1; -.  
DR HSSP; Q07817; IMAZ.  
DR MGD; MGI:108052; Bcl2l2.  
DR InterPro; IPR000712; Bcl2 BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SMC0337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 178 AA; 19147 MW; E2D4C3F79528E9D7 CRC64;

Query Match 75.6%; Score 761; DB 11; Length 178;  
Best Local Similarity 95.3%; Pred. No. 2.7e-60;  
Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
|||||  
Db 1 MATPASTPTDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
|||||

QY 61 FSDLAAQLHVTTPGSAQQRFTQVSDSELFQGGPNWGRJLVAFVFGAALCAESVNKEMEPLVG 120  
|||||  
Db 61 FSDLAAQLHVTTPGSAQQRFTQVSDSELFQGGPNWGRJLVAFVFGAALCAESVNKEMEPLVG 120  
|||||

QY 121 QVQEWMMVAYLETRLADWIHSSGGWAEFTAL 150  
|||||  
Db 121 QVQDMMVAYLETRLADWIHSSGGWVRSSQL 150  
|||||

RESULT 4  
Q8CFR2 PRELIMINARY; PRT; 178 AA.

ID Q8CFR2  
AC Q8CFR2;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Bcl2-like 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Eye;

RA Strausberg R.;

RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BCC40369; AAH40369.1; -

SQ SEQUENCE 178 AA; 19119 MW; E2C3F3F79528E9D7 CRC64;

Query Match: 75.6%; Score 761; DB 11; Length 178;

Best Local Similarity 95.3%; Pred. No. 2.7e-60;

Matches 143; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 MATPASAPDTRALVADFVGYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60

DB 1 MATPASTPDTRALVADFVGYKLRQKGYVCGAGGEGPAADPLHQAMRAAGDEFETRFRRT 60

QY 61 FSDLAQAQLHVTGPSAQCRFTQVSDLELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120

DB 61 FSDLAQAQLHVTGPSAQCRFTQVSDLELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120

QY 121 QVQEWXVAYLETRLADWIHSSGGWAEFTAJ 150

DB 121 QVQEWXVAYLETRLADWIHSSGGWVRSSQL 150

RESULT 5

Q9MYW4

ID Q9MYW4 PRELIMINARY; PRT; 233 AA.

AC Q9MYW4;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Bcl-X.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI\_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RA Knott J.C., Robertson L., James E.R.;

RT "Rabbit Bcl-X.";

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY005131; AAF88137.1; -

DR HSSP; P53563; IAF3.

DR InterPro; IPR000712; Bcl2\_BH.

DR InterPro; IPR003093; Bcl2\_BH4.

DR InterPro; IPR002475; BCL2\_family.

DR InterPro; IPR004725; Bcl2\_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4\_1; 1.

DR PROSITE; PS50063; BH4\_2; 1.

SQ SEQUENCE 233 AA; 25986 MW; 12F0F30344D53F93 CRC64;

Query Match: 43.7%; Score 440.5; DB 6; Length 233;

Best Local Similarity 42.0%; Pred. No. 1.7e-31;

Matches 94; Conservative 22; Mismatches 57; Indels 51; Gaps 4;

QY 11 RALVADFVGYKLRQKGYVC-----GAG-----PGECPAA 39

DB 6 RELVDFLSYKLSQKGYSWSQFSDVEENRTEAPEGTGEMETPSAINGNPAWHPADSPAV 65

QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAQAQLHVTGPSAQCRFTQ 81

DB 66 NGATGSSSLDAREVIPMTAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

QY 82 VSDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEWXVAYLETRLADWIHSS 141

DB 126 VVNELFRDGVNWGRIVAFVFGALCVESVDKEMEVLVSRIAAWMTYLNHLEPWIQEN 185

QY 142 GCWAEFTALYGDGALEEEARRLRE--GNWASVRTVLTGAVALGAL 183

DB 186 GGWDTFVELYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 6

C35844

ID C35844 PRELIMINARY; PRT; 233 AA.

AC C35844;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE Bcl-xL.

GN BCL2L.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=B6/CBA; TISSUE=Thymus;

RX MEDLINE=98051053; PubMed=9390687;

RA Yang X.-F., Weber G.F., Cantor H.;

RT "A novel Bcl-x isoform connected to the T cell receptor regulates

RT apoptosis in T cells.";

RL Immunity 7:629-639(1997).

DR EMBL; U51278; AAC53459.1; -

DR HSSP; P53563; IAF3.

DR MGD; MGI:88139; Bcl2l.

DR InterPro; IPR000712; Bcl2\_BH.

DR InterPro; IPR003093; Bcl2\_BH4.

DR InterPro; IPR002475; BCL2\_family.

DR InterPro; IPR004725; Bcl2\_reg.

DR Pfam; PF00452; Bcl-2; 1.

DR Pfam; PF02180; BH4; 1.

DR SMART; SM00337; BCL; 1.

DR SMART; SM00265; BH4; 1.

DR TIGRFAMs; TIGR00865; bcl-2; 1.

DR PROSITE; PS50062; BCL2\_FAMILY; 1.

DR PROSITE; PS01080; BH1; 1.

DR PROSITE; PS01258; BH2; 1.

DR PROSITE; PS01259; BH3; 1.

DR PROSITE; PS01260; BH4\_1; 1.

DR PROSITE; PS50063; BH4\_2; 1.

SQ SEQUENCE 233 AA; 26033 MW; 3083F2D8327E072E CRC64;

Query Match: 43.2%; Score 435.5; DB 11; Length 233;

Best Local Similarity 41.8%; Pred. No. 4.8e-31;

Matches 94; Conservative 22; Mismatches 56; Indels 53; Gaps 4;

QY 11 RALVADFVGYKLRQKGY-----V 28

DB 6 RELVDFLSYKLSQKGYSWSQFSDVEENRTEAPEETEAEETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGECPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAQAQLHVTGPSAQCRFT 80

DB 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

QY 81 QVSDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVGQVQEWXVAYLETRLADWIHS 140

DB 125 QVVNELFRDGVNWGRIVAFVFGALCVESVDKEMEVLVSRIASWMTYLNHLEPWIQIE 184

QY 141 SGGWAEFTALYGDGALEEEARRLREG--NWASVRTVLTGAVALGAL 183

DB 185 NGGWDTFVDLYGNNAAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 7

Q8SQ42

ID Q8SQ42 PRELIMINARY; PRT; 233 AA.

AC Q8SQ42;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Bcl-x1 protein.  
GN BCL-XL.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;  
RT "Molecular cloning of feline Bcl-2 family."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB080951; BAB85856.2; --  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;  
  
Query Match 43.0%; Score 433.5; DB 6; Length 233;  
Best Local Similarity 41.6%; Pred. No. 7.3e-31;  
Matches 97; Conservative 23; Mismatches 58; Indels 55; Gaps 5;  
  
QY 11 RALVADFVGKLRQKGY-----V 28  
D 6 RELVVDFLSYKLSQKGSWSRFSFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65  
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQORFT 80  
D 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124  
QY 81 QVSDELFQGGPNWGRVLVAFFVFGAALCAESVKNKEMPLVGQVCEWMVAYLETRLADWIHS 140  
D 125 QVNVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRATWMTATYLNCHLEPWIQE 184  
QY 141 SGGWAEFTALYGDGALEEARLRREGNWSVRVTLTGAVAGALVTVGAFASK 193  
D 185 NGGWDTFVELYGNNAEAESRK--GQERSNRWFLTGMTVAG-VLLGSLFSRK 233  
  
RESULT 8  
Q9N1A2 PRELIMINARY; PRT; 233 AA.  
AC Q9N1A2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anti-apoptotic regulator Bcl-XL.  
GN BCL-XL.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Lee T.L., Canty J.M.;  
RT "PCR Cloning of a Porcine bcl-xL cDNA from Heart."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF216205; AAF33212.1; --  
DR HSSP; Q07817; IMAZ.

DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;  
  
Query Match 42.9%; Score 431.5; DB 6; Length 233;  
Best Local Similarity 41.8%; Pred. No. 1.1e-30;  
Matches 94; Conservative 21; Mismatches 57; Indels 53; Gaps 4;  
  
QY 11 RALVADFVGKLRQKGY-----V 28  
D 6 RELVVDFLSYKLSQKGSWSQFTDVENRTEAPEGTESEAEPTSAINGNPSWHLADSPAV 65  
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQORFT 80  
D 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124  
QY 81 QVSDELFQGGPNWGRVLVAFFVFGAALCAESVKNKEMPLVGQVCEWMVAYLETRLADWIHS 140  
D 125 QVNVNELFRDGVNWGRIVAFFSFGGALCVESVDKEMQVLVSRATWMTATYLNCHLEPWIQE 184  
QY 141 SGGWAEFTALYGDGALEEARLRREGNWSVRVTLTGAVAGAL 183  
D 185 NGGWDTFVELYGNNAEAESRKQBERFNRWFLTGMTLAGVVLGSL 229  
  
RESULT 9  
Q9MZS7 PRELIMINARY; PRT; 233 AA.  
AC Q9MZS7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Bcl-x long protein.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;  
RT "Bcl-x in the sheep ovary."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF164517; AAF89532.1; --  
DR HSSP; P53563; IAF3.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.

DR PROSITE; PS50063; BH4 2; 1.  
SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;  
  
Query Match 42.6%; Score 428.5; DB 6; Length 233;  
Best Local Similarity 40.6%; Pred. No. 2e-30;  
Matches 91; Conservative 23; Mismatches 59; Indels 51; Gaps 4;  
  
Qy 11 RALVADFVGYKLRQKGY-----PLHQAMRAAGDEFETFRRTFSDLAALHVTTPGSAQQRFTQ 81  
Db 6 RELVVDFLSYKLSQKGSWSQFSDVENRTEAPEGETSDMETPSAINGNFSWHLADSPAV 65  
  
Qy 40 D-----PLHQAMRAAGDEFETFRRTFSDLAALHVTTPGSAQQRFTQ 81  
Db 66 NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHTTPGTAYQSFEQ 125  
  
Qy 82 VSDELFGQGNWGRVLVAFFVFGAALCAESVNKEMEPVGVQVQVEMVAYLETRLADWIHSS 141  
Db 126 VVNELFRDGVNWGRIVAFFSPGALCVESVDKEMQVLVSRIATWMTATYLDNDHLEPWIQEN 185  
  
Qy 142 GGWAETALYGDGALEEARLRE--GNWASVRTVLTGVALGAL 183  
Db 186 GGWDTFVELYGNNAABESRKQERFNRWFLTGMTVAGVVLGSL 229  
  
RESULT 10  
Q8BQK4  
ID Q8BQK4 PRELIMINARY; PRT; 236 AA.  
AC Q8BQK4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE B-cell leukemia/lymphoma 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Body;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK049473; BAC33767.1; --  
SQ SEQUENCE 236 AA; 26437 MW; B726BFFA3AA1C718 CRC64;  
  
Query Match 41.0%; Score 413; DB 11; Length 236;  
Best Local Similarity 37.5%; Pred. No. 5e-29;  
Matches 87; Conservative 34; Mismatches 59; Indels 52; Gaps 5;  
  
Qy 9 DTRALVADFVGYKLRQKGYVCGAG-----PG----- 34  
Db 10 DNREIVMKYIHYKLSQRGYWDAGDADAAPLGAAPTGGIFSFPQESNPMPAVHRDVAART 69  
  
Qy 35 -----EGPAADP-----LHQAMRAAGDEFETFRRTFSDLAALHVTTPGSAQQRFTQ 81  
Db 70 SPLRPLVATTGPALSPVPPVPHLTLRAGDDFSRRYRDDFAEMSSQLHLPFTARGFAT 129  
  
Qy 82 VSDELFGQGNWGRVLVAFFVFGAALCAESVNKEMEPVGVQVQVEMVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNWGRIVAFFEFGVMCVESVNREMSPLVDNIALWMTYLNRLHTWIQDN 189  
  
Qy 142 GGWAETALYGDGALEEARLRREGNWNASVRTVLTGVALGALVTVGAFASK 193  
Db 190 GGWDARVELYG----PSMRPLDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236  
  
RESULT 11  
Q90Z98  
ID Q90Z98 PRELIMINARY; PRT; 238 AA.  
AC Q90Z98;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Bcl-XL-like protein 1.  
GN BCL2L OR BLP1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21299061; PubMed=11406282;  
RA Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.-L.;  
RT "Cloning and characterization of zfBLP1, a Bcl-XL homologue from the  
RT zebrafish, Danio rerio(1).";  
RL Biochim. Biophys. Acta 1519:127-133 (2001).  
DR EMBL; AF317837; AAK81706.1; --  
DR ZFIN; ZDB-GENE-010730-1; bcl2l.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDDB CRC64;  
  
Query Match 40.0%; Score 403; DB 13; Length 238;  
Best Local Similarity 36.6%; Pred. No. 4e-28;  
Matches 87; Conservative 27; Mismatches 62; Indels 62; Gaps 6;  
  
Qy 11 RALVADFVGYKLRQKGYVC-----GAG----- 32  
Db 6 RELVVFYIKYKLSQRNYPCHGLTETNRTDGAENGEGAGATLVNGTNRTNASST 65  
  
Qy 33 --PGECPAADPLHQ-----AMRAAGDEFETFRRTFSDLAALHVTTPGSAQQR 78  
Db 66 GTPPQSPASSPQRQTNGSGGLDAVKEALRDSANEFELRYSRAFNDLSSQLHITPATAYQS 125  
  
Qy 79 FTQVSDDELFGQGNWGRVLVAFFVFGAALCAESVNKEMEPVGVQVQVEMVAYLETRLADWI 138  
Db 126 FESWDEVRDGVNWGRIVGLFAFGGALCVCEVEKEMSPVLGVRIAEWMTVYLGNHIQPI 185  
  
Qy 139 HSSGGWAEFTALYGDGALEEARLRREG--NNA-SVRTVLTGVALGALVTVGAFASK 193  
Db 186 QSQGWERFAEIFGKDAABESRKQESFKKMLFAGMTLLTG-----VVVGGGLIAOK 236  
  
RESULT 12  
Q9BDD5  
ID Q9BDD5 PRELIMINARY; PRT; 180 AA.  
AC Q9BDD5;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anti-apoptotic regulator Bcl-XL (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Amills M., Bouzat J.;  
RT "Characterization of the bovine bcl-xL gene and related pseudogenes."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF245488; AAK31307.1; --  
DR EMBL; AF245489; AAK31308.1; --  
DR HSSP; Q07817; 1MAZ.  
DR InterPro; IPR000712; Bcl2\_BH.



DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SMC0337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
FT NON\_TER 180 180  
SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;  
  
Query Match 39.8%; Score 401; DB 6; Length 180;  
Best Local Similarity 53.5%; Pred. No. 4.2e-28;  
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;  
  
QY 44 QAMRAAGDEFETRFRRTFSDLAALHVTGPSAQORFTQVSDQLFQGGPNWGRVLVAFVFG 103  
Db 38 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFQVWVNELFRDGVNWGRIVAFVFG 97  
  
QY 104 AALCAESVNKEMEPLVGVQVQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLR 163  
Db 98 GALCVESVDKEMQVLVSRIATWMTYLNHDHLEPWIQENGWDTFVELYGNNAAESRKGG 157  
  
QY 164 E--GNWASVRTVLTGAVALGAL 183  
Db 158 ERFNRWFLTGMTVAGVVLGSL 179  
  
RESULT 13  
Q99N35  
-D Q99N35 PRELIMINARY; PRT; 217 AA.  
AC Q99N35;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE B-cell leukemia/lymphoma x (Fragment).  
GN BCLX.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SVJ;  
RA Yang X.-F., Cantor H.;  
RT "Novel cDNA structure and genomic organization of apoptosis regulatory  
RT gene Bcl-x-gamma.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF133282; AAK15455.1; -.  
DR EMBL; AF133281; AAK15455.1; JOINED.  
DR HSSP; P53563; 1AF3.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; BCL2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 217 AA; 24234 MW; 3B5A4E809A7DEF18 CRC64;  
  
Query Match 39.8%; Score 401; DB 11; Length 217;  
Best Local Similarity 53.5%; Pred. No. 5.4e-28;  
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;  
  
QY 44 QAMRAAGDEFETRFRRTFSDLAALHVTGPSAQORFTQVSDQLFQGGPNWGRVLVAFVFG 103  
Db 72 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFQVWVNELFRDGVNWGRIVAFVFG 131  
  
QY 104 AALCAESVNKEMEPLVGVQVQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLR 163

Db 132 GALCVESVDKEMQVLVSRIASWMTYLNHDHLEPWIQENGWDTFVCLYGNNAAESRKGG 191  
QY 164 E--GNWASVRTVLTGAVALGAL 183  
Db 192 ERFNRWFLTGMTVAGVVLGSL 213  
  
RESULT 14  
Q923R6  
ID Q923R6 PRELIMINARY; PRT; 236 AA.  
AC Q923R6;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)  
DE B-cell lymphoma protein 2.  
GN BCL2.  
OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
CC Cricetulus.  
CX NCBI\_TaxID=10030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai D.Z., Chen W., Wang H.T.;  
RT "Construction of a robust CHO cell line for biopharmaceutical use";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF404339; AAK92201.1; -.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 236 AA; 26500 MW; BEDF052EFF32CA8B8 CRC64;  
  
Query Match 39.6%; Score 399; DB 11; Length 236;  
Best Local Similarity 35.3%; Pred. No. 9e-28;  
Matches 82; Conservative 32; Mismatches 66; Indels 52; Gaps 3;  
  
QY 9 DTRALVADFVGKLRQKGY-----  
Db 10 DNREIVMKYIHYKLSQRGYWDVGVDAAPLGAAPTGFISFQPSNPTPAVHRDMAART 69  
QY 28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAALHVTGPSAQORFTQ 81  
Db 70 SPLRPVATTGPTLSPPVPPVHLLTRRAGDDFSRRYRRDFAEMSSQLHLPFTARGRFAT 129  
QY 82 VSDELFOGGPNWGRVLVAFVFGAALCAESVNKEMEPLVGVQVQEWVAYLETRLADWIHSS 141  
Db 130 VVEELFRDGVNWGRIVAFVFGGVMCVESVNREMSPLVDNIALMWTYLNRLHHTWIQDN 189  
QY 142 GGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVALGALVTVGAFFASK 193  
Db 190 GGWDAFVELYG----PSVRPLDFSWLSLXTLLNAL-VGACITLGTYLGHK 236  
  
RESULT 15  
Q9BDX7  
ID Q9BDX7 PRELIMINARY; PRT; 180 AA.  
AC Q9BDX7;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)



DE Anti-apoptotic regulator Bcl-xL (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Axillis M., Bouzat J.;  
RT "Characterization of the bovine bcl-xL gene and related pseudogenes.";  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF245487; AAK31306.1; -.  
DR HSSP; Q07817; 1MAZ.  
DR InterPro; IPR000712; BCL2 BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PSS0062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
FT NON\_TER 180  
SQ SEQUENCE 180 AA; 20056 MW; 62C4C0BD0555A9EF CRC64;  
  
Query Match 39.6%; Score 398.5; DB 6; Length 180;  
Best Local Similarity 47.1%; Pred. NC. 7.e-28;  
Matches 82; Conservative 23; Mismatches 58; Indels 11; Gaps 3;  
  
QY 20 YKLRQKGYVCGAGGEGSPAAD-----PLHQAAMRAAGDEFETFRFTFSDLAAQLHVT 71  
DB 7 WHLEDSPAVNGA-PGHSRSSDAREVIPMAAVKQALREAGDEFELRYKRAFSDLTSQLHIT 65  
  
QY 72 PGSAQQRFTQVSDLEFQGPNGRLVAFFVFGAALCAESVKNKEMEPLVGQVQEWVAYLE 131  
DB 66 PGTAYQSFEQVNVNELFRDGNWGRIVASFSGGALCVESVCKEMQVLVSRIATWTMATYLN 125  
  
QY 132 TRLDADWIHSSGGWAEFTALYGDGALEEARLRE--GNWASVRTVLTGVALGAL 183  
DB 126 DHLEPWIQENGWDTFVELYGNNAAESRKQGRFNRWFLTGMTVAGVVLGSL 179

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:03:45 ; Search time 1737.99 Seconds  
(without alignments)  
13722.924 Million cell updates/sec

Title: US-09-925-674A-6  
Perfect score: 583  
Sequence: 1 atggcgacccagcctcgcc.....ctttttgctagcaagtga 583

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2889711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_htg:\*
- 3: gb\_in:\*
- 4: gb\_om:\*
- 5: gb\_ov:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
- 20: em\_om:\*
- 21: em\_or:\*
- 22: em\_ov:\*
- 23: em\_pat:\*
- 24: em\_ph:\*
- 25: em\_pl:\*
- 26: em\_ro:\*
- 27: em\_sts:\*
- 28: em\_un:\*
- 29: em\_vi:\*
- 30: em\_htg\_hum:\*
- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_mus:\*
- 34: em\_htg\_pln:\*
- 35: em\_htg\_rod:\*
- 36: em\_htg\_mam:\*
- 37: em\_htg\_vrt:\*
- 38: em\_sy:\*
- 39: em\_htgc\_hum:\*
- 40: em\_htgo\_mus:\*
- 41: em\_htgo\_other:\*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match %	Length	DB	ID	Description
1	582	99.8	582	6	AX481423	AX481423 Sequence
2	582	99.8	582	9	HSU59747	U59747 Human Bcl-w
3	579.8	99.5	3542	9	D87461	D87461 Human mRNA
4	578.2	99.2	583	6	AX022529	AX022529 Sequence
5	578.2	99.2	583	6	AX030817	AX030817 Sequence
6	578.2	99.2	1437	9	BC021198	BC021198 Homo sapi
7	572.6	98.2	579	6	AR020780	AR020780 Sequence
8	532.4	91.3	582	10	AF096291	AF096291 Rattus no
9	527.8	90.5	579	6	AR020779	AR020779 Sequence
10	527.6	90.5	582	10	MMU59746	U59746 Mus musculu
11	527.6	90.5	3476	10	AF030769	AF030769 Mus muscu
12	516.4	88.6	3473	10	AY170344	AY170344 Mus muscu
13	505.8	86.8	581	6	AX022531	AX022531 Sequence
14	505.8	86.8	581	6	AX030819	AX030819 Sequence
15	446	76.5	220818	2	AC128940	AC128940 Rattus no
16	446	76.5	223933	2	AC097389	AC097389 Rattus no
17	428.8	73.6	1098	6	BD078624	BD078624 Human pro
18	428.2	73.4	196292	9	CNS0000B	ALC49829 Human chr
19	388.6	66.7	148278	2	AC079885	AC079885 Rattus no
20	388.6	66.7	180665	2	AC084240	AC084240 Rattus no
21	388.6	66.7	221557	2	AC134055	AC134055 Rattus no
22	386.6	66.3	210784	2	AC119293	AC119293 Rattus no
23	386.6	66.3	263901	2	AC115371	AC115371 Rattus no
24	380.2	65.2	3815	10	BC040369	BC040369 Mus muscu
25	380.2	65.2	237561	10	AC116591	AC116591 Mus muscu
26	257	44.1	6049	6	AX345130	AX345130 Sequence
27	239.8	41.1	749	5	XLR1	X82462 X.laavis RI
28	223	38.3	6049	6	AX345131	AX345131 Sequence
29	143	24.5	764	10	RNU10579	U10579 Rattus norv
30	143	24.5	1742	6	BD012974	BD012974 A mutagen
31	143	24.5	1742	6	BD013799	BD013799 Modified
32	143	24.5	1742	10	RNU72350	U72350 Rattus norv
33	143	24.5	2232	10	RNCBLXLS	X82537 R.norvegicu
34	142.2	24.4	1252	4	AB073983	AB073983 Canis fam
35	140.6	24.1	1163	4	AB080951	AB080951 Felis cat
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39	135.8	23.3	766	4	AF164517	AF164517 Ovis arie
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43	133.8	23.0	695	6	AX525912	AX525912 Sequence
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45	132.8	22.8	702	10	MMU10101	U10101 Mus musculu

ALIGNMENTS

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AX481423	LOCUS	AX481423				
DEFINITION	AX481423					
ACCESSION	AX481423					
VERSION	AX481423.1	GI:22316337				
KEYWORDS						
SOURCE						
ORGANISM						
REFERENCE						
AUTHORS						
TITLE						
JOURNAL						

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Best Local Similarity 100.0%; Pred. No. 1.2e-120;  
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DB 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
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DB 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGCTGGCACTG 540  
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DB 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTCTAGCAAGTGA 582  
RESULT 2  
HSU59747  
LOCUS HSU59747 582 bp mRNA linear PRI 29-SEP-1996  
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.  
ACCESSION U59747  
VERSION U59747.1 GI:1572492  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 582)  
AUTHORS Gibson, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,  
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.  
bcl-w, a novel member of the bcl-2 family, promotes cell survival  
Oncogene 13 (4), 665-675 (1996)  
MEDLINE 96358615  
PUBMED 8761287  
REFERENCE 2 (bases 1 to 582)

AUTHORS Gibson, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and  
Cory, S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and  
Eliza Hall Institute of Medical Research, PO Royal Melbourne  
Hospital, Parkville, Victoria 3050, Australia  
FEATURES Location/Qualifiers  
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CDS 1..582  
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BASE COUNT 104 a 156 c 211 g 111 t  
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Query Match 99.8%; Score 582; DB 9; Length 582;  
Best Local Similarity 100.0%; Pred. No. 1.2e-120;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
DB 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
QY 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
DB 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
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DB 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTCTAGCAAGTGA 582

RESULT 3  
D87461  
LOCUS  
DEFINITION Human mRNA for KIAA0271 gene, complete cds.  
ACCESSION D87461  
VERSION D87461.1 GI:1944417  
KEYWORDS KIAA0271.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE  
AUTHORS Nagase,T., Seki,N., Ishikawa,K., Chira,M., Kawarabayashi,Y.,  
Chara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.  
TITLE Prediction of the coding sequences of unidentified human genes. VI.  
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
analysis of cDNA clones from cell line KG-1 and brain  
JOURNAL DNA Res. 3 (5), 321-329 (1996)  
MEDLINE 97191544  
PUBMED 9039502  
REFERENCE  
AUTHORS Chara,O., Nagase,T., Kikuno,R. and Nomura,N.  
TITLE Direct Submission  
JOURNAL Submitted (27-AUG-1996) Osamu Chara, Kazusa DNA Research Institute;  
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-439-52-3913)  
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source  
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Query Match 99.5%; Score 579.8; DB 9; Length 3542;  
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Matches 581; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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RESULT 4  
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LOCUS Sequence 6 from Patent EP0932674.  
ACCESSION AX022529  
VERSION AX022529.1 GI:10046125  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE unclassified.  
1  
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
apoptosis-controlling genes  
JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;  
AMRAD OPERATIONS PTY LTD (AU)  
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BASE COUNT 105 a 157 c 210 g 111 t  
ORIGIN  
Query Match 99.2%; Score 578.2; DB 6; Length 583;  
Best Local Similarity 99.5%; Pred. No. 8.5e-120;  
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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DEFINITION Sequence 6 from Patent WO9735971.  
ACCESSION AX030817  
VERSION AX030817.1 GI:10278311

KEYWORDS  
SOURCE unidentifed  
ORGANISM unidentifed  
unclassified.

REFERENCE 1  
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
apoptosis-controlling genes  
JOURNAL Patent: WO 9735971-A 6 02-OCT-1997;  
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAWN P (AU) ; CORY SUZANNE (AU)  
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)

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BASE COUNT 105 a 157 c 210 g 111 t  
ORIGIN

Query Match 99.2%; Score 578.2; DB 6; Length 583;  
Best Local Similarity 99.5%; Pred. No. 8.5e-120;  
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60  
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RESULT 6  
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DEFINITION Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,  
complete cds.

ACCESSION BC021198  
VERSION BC021198.1 GI:10203706  
KEYWORDS MGC.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Strausberg,R.  
TITLE Direct Submission  
JOURNAL Submitted (14-JAN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNz)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc.mgc@nhgri.nih.gov

Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,  
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,  
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,  
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,  
Tiongson,B.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,



Zhang, L.-H. and Green, S.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 15 Row: k Column: 19  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 14574571.

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LOCUS      AR020780              579 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 2 from patent US 5789201.
ACCESSION  AR020780
VERSION     AR020780.1  GI:3975395
KEYWORDS    .
SOURCE      Unknown.
ORGANISM    Unknown.
REFERENCE   1 (bases 1 to 579)
AUTHORS     Guastella,J.
TITLE       Genes coding for bcl-y a bcl-2 homologue
JOURNAL     Patent: US 5789201-A 2 04-AUG-1998;
            Location/Qualifiers
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RESULT 8
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LOCUS      AF096291              582 bp      mRNA      linear      ROD 28-FEB-2000
DEFINITION Rattus norvegicus Bcl-w (bcl-w) mRNA, complete cds.
ACCESSION  AF096291
VERSION     AF096291.1  GI:3747129
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KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 582)  
AUTHORS Hamner,S., Skoglosa,Y. and Lindholm,D.  
TITLE Differential expression of bcl-w and bcl-x messenger RNA in the  
developing and adult rat nervous system  
JOURNAL Neuroscience 91 (2), 673-684 (1999)  
MEDLINE 99292146  
PUBMED 10366024  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Hamner,S., Skoglosa,Y. and Lindholm,D.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-1998) Developmental Neuroscience, Uppsala  
University, Box 587, BMC, Uppsala 751 23, Sweden  
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Query Match 91.3%; Score 532.4; DB 10; Length 582;  
Best Local Similarity 94.7%; Pred. No. 1.7e-109;  
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LOCUS AR020779 579 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 1 from patent US 5789201.  
ACCESSION AR020779  
VERSION AR020779.1 GI:3975394  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 579)  
AUTHORS Guastella,J.  
TITLE Genes coding for bcl-y a bcl-2 homologue  
JOURNAL Patent: US 5789201-A 1 04-AUG-1998;  
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ORIGIN  
Query Match 90.5%; Score 527.8; DB 6; Length 579;  
Best Local Similarity 94.5%; Pred. No. 1.9e-108;  
Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
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LOCUS	MMU59746	582 bp	mRNA linear ROD 29-SEP-1996
DEFINITION	Mus musculus Bcl-w (bcl-w) mRNA, complete cds.		
ACCESSION	U59746		
VERSION	U59746.1	GI:1572494	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	1 (bases 1 to 582) Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., Copeland,N.G., Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.		
TITLE	bcl-w, a novel member of the bcl-2 family, promotes cell survival		
JOURNAL	Oncogene 13 (4), 665-675 (1996)		
MEDLINE	96358615		
PUBMED	8761287		
REFERENCE	2 (bases 1 to 582)		
AUTHORS	Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.M. and Cory,S.		
TITLE	Direct Submission		
JOURNAL	Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia		
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QY	61	AAGCTGAGGCAGAGGGTTATGCTGTGGAGCTGGCCCGGGAGGGCCCGCAGCAGTGAC	120
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QY	121	CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTTCAGACCCCGCTTCGGCGCACC	180
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QY	181	TTCTCTGATCTGGCGGCTCAGCTGCATGTGTACCCCGAGGCTCAGCCCGCAGCAACGGCTCACC	240
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QY	241	CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCCGCTTGTAGCCTCTTT	300
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DEFINITION	Mus musculus BCL-W (Bcl-w) mRNA, complete cds.		
ACCESSION	AF030769		
VERSION	AF030769.1	GI:2623249	
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
AUTHORS	1 (bases 1 to 3476) Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and MacGregor,G.R.		
TITLE	Bcl-w is required for testis homeostasis		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 3476)		
AUTHORS	Ross,A.J. and MacGregor,G.R.		
TITLE	Direct Submission		
JOURNAL	Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA		
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Best Local Similarity 94.2%; Pred. No. 1.6e-108;  
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RESULT 12  
AY170344 3473 bp mRNA linear RCD 04-JAN-2003  
LOCUS Mus musculus Bcl2-like protein 2 mRNA, complete cds.  
DEFINITION AY170344  
ACCESSION  
VERSION AY170344.1 GI:27497698  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3473)  
AUTHORS Su,H.-Y.  
TITLE Extraction from neonatal mouse skin after IGF-1 stimulation

JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3473)  
AUTHORS Su,H.-Y.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1,  
Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan  
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Db 476 GTCTTTGGGGCTGCCCTGTGTGAGAGAGTGTCAACAAGAANAATGGAGCCTTTSGTGGGA 535  
QY 361 CAAGTGAGGAGTGGATGGTGGCTACCTGGAGACGGCGCTGGCTGACTGGATCCACAGC 420  
|||||  
Db 536 CAAGTGAGGATTTGGATGGTGGCTACCTGGAGACACGCTCTGGCTTACTGGATCCACAGC 595  
QY 421 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGCGG 480  
|||||  
Db 596 AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGACGG 655  
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|||||  
Db 656 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 715  
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Dc 421 AGTGGCGGCTGGGCGGACTTCACAGCTCTATACGGGACGGGGCCCTGGAGGACGCACGG 480

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Dc 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTG 540

Qy 541 GGGGCCCTGGTAACCTGTAGGGCCCTTTTTCCTAGCAAGTG 581

Dc 541 GGGGCCCTGGTAACCTGTAGGGCCCTTTTTCCTAGCAAGTG 581

RESULT 15

AC128940

LOCUS

DEFINITION Rattus norvegicus clone CH230-43402, \*\*\* SEQUENCING IN PROGRESS

\*\*\* 4 unordered pieces.

AC128940

AC128940.3 GI:25073546

HTG: HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.

KEYWORDS Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1 (bases 1 to 220818)

Muzny,D.,Marie., Metzker,M.,Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Fallis,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogue,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,J., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayer,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,D., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwonu,G., Oiarunpungo,A., Pat.S., Parks,X., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Popper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,

Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

2 (bases 1 to 220818)

Worley,K.C.

Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 220818)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23269386.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

----- Project Information

Center project name: KBEM

Center clone name: CH230-43402

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 202395 bases at least Q40

Consensus quality: 205627 bases at least Q30

Consensus quality: 207823 bases at least Q20

Estimated insert size: 212631; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 4 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

\* 1 174472: contig of 174472 bp in length

\* 174473 174572: gap of unknown length

\* 174573 218266: contig of 43694 bp in length

\* 218267 218366: gap of unknown length

\* 218367 219597: contig of 1231 bp in length

\* 219598 219697: gap of unknown length

\* 219698 220818: contig of 1121 bp in length.

Location/Qualifiers

1..220818

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-43402"

28851..30762

/note="wgs contig"

misc\_feature 62390 a 42027 c 41606 g 62941 t 11854 others

BASE COUNT 62390 a 42027 c 41606 g 62941 t 11854 others

ORIGIN

Query Match 76.5%; Score 446; DB 2; Length 220818;

Best Local Similarity 87.1%; Pred. No. 2.le-90;									
Matches 507; Conservative 0; Mismatches 60; Indels 15; Gaps 1;									
Qy	1	ATGGCGACCCAGCCTCGGCCGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT	60						
Db	141986	ATGGCAATCCAGTCTCAACCCGACACACATGGGCTCTAGTGGCTGACTTTGTAGGCTAT	142045						
Qy	61	AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCGAGCAGCTGAC	120						
Db	142046	AAGCTGAGGTAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGAAAGGCCGACAGCTGAT	142105						
Qy	121	CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTCGAGACCCGCTTCCGGCGCACC	180						
Db	142106	CTGCTACACCAAGCCATGCTGTCTGGAGACGAGTTTGAGACCCGCTTCCGGTACACC	142165						
Qy	181	TTCTCTGATCTGCGGGCTCAGCTGCATGTGACCCCGGCTCAGCCGACCAACGCTTCACC	240						
Db	142166	TTCTCTGACCTAGCCACTCAGCAACATGTGACCCGAGGCTCAGCCGACCAACGCTTCACC	142225						
Qy	241	CAGGTCTCCGACGAACTTTTCAAGGGGGCCCCAACTGGGGCGCCCTTGTAGCCTTCTTT	300						
Db	142226	CAGGTTCCGATGAACTTTTCAAGGGGGCCCCAACTGGGGACGTCCTTGTGGCATCTCT	142285						
Qy	301	GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA	360						
Db	142286	GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGGCATTGGTGGGA	142345						
Qy	361	CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGGTGGCTGACTGGATCCACAGC	420						
Db	142346	CAAGTGCAGGACTGGATGGTGGCTACCTGGAGACATGCCTGACTGACTGGATCGACAGC	142405						
Qy	421	AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGCGG	480						
Db	142406	AGTGGGGCTGGGTGGAGTTCACAGCTCAATACGAGGACGGGGCCCTGGAGGAGGTAC--	142463						
Qy	481	CGTCTGCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGGCCGTGGCACTG	540						
Db	142464	-----GGAACTGAGCATCAGTGAGGATAGTGTGATGGGGCTGTGGCACTA	142510						
Qy	541	GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAGTGA	582						
Db	142511	GGAGCCCTGGTAACCTGTAGGGGCCCTTTTGTAGCTAGCAASTGA	142552						

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:02:30 ; Search time 177.152 Seconds  
(without alignments)  
8883.744 Million cell updates/sec

Title: US-09-925-674A-6  
Perfect score: 583  
Sequence: 1 atggcgacccagcctcggc.....cttttttgctagcaagtga 583

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*  
1: /SIDS1/gcgdata/geneseq/geneseq-embl/NA1980.DAT:\*  
2: /SIDS1/gcgdata/geneseq/geneseq-embl/NA1981.DAT:\*  
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6: /SIDS1/gcgdata/geneseq/geneseq-embl/NA1985.DAT:\*  
7: /SIDS1/gcgdata/geneseq/geneseq-embl/NA1986.DAT:\*  
8: /SIDS1/gcgdata/geneseq/geneseq-embl/NA1987.DAT:\*  
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23: /SIDS1/gcgdata/geneseq/geneseq-embl/NA2001B.DAT:\*  
24: /SIDS1/gcgdata/geneseq/geneseq-embl/NA2002.DAT:\*  
25: /SIDS1/gcgdata/geneseq/geneseq-embl/NA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582	99.8	582	24	ABZ35729 Human bcl-w polynu
2	582	99.8	582	24	ABX09972 Human bcl-w DNA fr
3	582	99.8	582	24	ABV78153 Human bcl-w DNA SE
4	582	99.8	582	24	ABL91694 Human polynucleoti
5	579.8	99.5	3542	25	ABT16642 Human bcl-2 gene S
6	578.2	99.2	583	18	AAT96577 Human bcl-w DNA.
7	578.2	99.2	583	20	AAZ25134 Human bcl-w gene d
8	577.8	99.1	581	20	AAZ25132 Human bcl-w gene.

9	572.6	98.2	579	19	AAV283334	Humar. bcl-y gene.
10	572.6	98.2	579	20	AAZ15946	cDNA encoding the
11	527.8	90.5	579	19	AAV283333	Rat bcl-y gene. R
12	527.8	90.5	579	20	AAZ15945	cDNA encoding the
13	526.6	90.3	581	20	AAZ25133	Mouse bcl-w gene.
14	505.8	86.8	581	18	AAT96578	Mouse bcl-w DNA.
15	505.8	86.8	581	20	AAZ25135	Mouse bcl-w gene d
16	428.8	73.6	1098	19	AAV41925	Nucleotide sequenc
17	428.4	73.5	1864	19	AAV59630	Human secreted pro
18	428.4	73.5	1864	24	ABS73617	Human cDNA #1 for
19	257	44.1	6049	24	ABL32228	Human immune syste
20	223	38.3	6049	24	ABL32229	Human immune syste
21	150	25.7	150	22	ABA47382	Human breast cell
22	150	25.7	150	22	ABA65269	Human foetal liver
23	150	25.7	150	22	ABA32370	Probe #10836 for g
24	150	25.7	150	22	AAK13683	Human brain expres
25	150	25.7	150	22	AAK39424	Human bone marrow
26	150	25.7	150	22	AAI20236	Probe #10169 for g
27	150	25.7	150	22	AAI45438	Probe #14124 used
28	150	25.7	150	22	AAI05940	Probe #5931 used
29	150	25.7	150	23	ABS39016	Human liver single
30	150	25.7	150	24	ABS13513	Human genome-deriv
31	143	24.5	1742	22	AAZ75960	Rat wiid-type Bcl-
32	133.8	23.0	695	24	ABT09346	Phase-1 Rat CT gen
33	131	22.5	636	22	AAH48169	Mutant bcl-XL codi
34	131	22.5	702	22	AAH43464	cDNA clone HP03564
35	131	22.5	926	16	AAQ81698	Human thymus BCL-X
36	131	22.5	926	17	AAT40079	Bcl-XL gene. Homo
37	131	22.5	926	21	AAZ93614	Bcl-x gene. Homo
38	131	22.5	926	22	AAS15189	Human bcl-x cDNA.
39	131	22.5	926	22	AAC90810	Human Bcl-XL nucle
40	131	22.5	926	24	ABK84766	Human cDNA differe
41	131	22.5	926	25	ABT16641	Human bcl-2 gene S
42	131	22.5	1236	22	AAS00247	Bcl-XL-DTR apoptos
43	131	22.5	7372	20	AAZ33182	Base sequence of t
44	128.6	22.1	660	24	ABT09345	Phase-1 Rat CT gen
45	128.2	22.0	720	22	AAH45295	DNA encoding human

ALIGNMENTS

RESULT 1

ABZ35729	ABZ35729	standard; DNA; 582 BP.
ID	ABZ35729	standard; DNA; 582 BP.
XX	ABZ35729	
AC	ABZ35729	
XX	07-FEB-2003	(first entry)
DC	Human bcl-w polynucleotide SEQ ID NO 37.	
XX	Double stranded RNA; dsRNA; RNAi; RNA inhibition; cytostatic; virucide;	
DE	protozoacide; gene expression; antisense; tumour; infection; Plasmodium;	
XX	virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;	
KW	Hepatitis C virus; human papilloma virus; gene; ds.	
XX	Homo sapiens.	
OS	DE10100588-A1.	
XX	18-JUL-2002.	
PD	09-JAN-2001; 2001DE-1000588.	
XX	09-JAN-2001; 2001DE-1000588.	
PR	(RIBO-) RIBOPHARMA AG.	
XX	Kreutzter R, Limmer S, Rost S, Hadwiger P;	
PA	WP-; 2002-683450/74.	
XX		



PT Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are  
PT complementary to the target -  
XX  
PS Claim 13; Page 30-31; 100pp; German.  
XX  
XX The invention relates to inhibiting expression of a target gene in a cell  
CC by introducing at least two oligoribonucleotides (dsRNAI and II), both  
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least part of one strand (S1, S2) of the ds structures in each  
CC of dsRNAI and II are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumours  
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is  
CC improved and efficiency can be increased further by pretreating the cells  
CC with interferon. The present sequence is that of a target DNA of the  
CC invention.  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match 99.8%; Score 582; DB 24; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.7e-135;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGGACCCAGCCCTCGGCCCCAGACACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
Db 1 ATGGGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
QY 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCACC 180  
Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCACC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGCTGAGTTCAGCCAGCAACGCTTCACC 240  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGCTGAGTTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGCGCTTGTAGCCTTCTTT 300  
Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGCGCTTGTAGCCTTCTTT 300  
QY 301 GTCTTTGGGGCTGCACCTGTGTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Db 301 GTCTTTGGGGCTGCACCTGTGTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
QY 361 CAAGTGACGAGTGGATGGTGGCCCTACCTGGAGACGCGGTGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGACGAGTGGATGGTGGCCCTACCTGGAGACGCGGTGCTGACTGGATCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGGCGCGG 480  
Db 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGACCGGGCCCTGGAGGAGGCGCGG 480  
QY 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGCACTG 540  
Db 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGCACTG 540  
QY 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAGTGA 582  
Db 541 GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAGTGA 582

RESULT 2  
ABX09972  
ID ABX09972 standard; DNA; 582 BP.  
XX

AC ABX09972;  
XX  
D- 23-JAN-2003 (first entry)  
XX  
DE Human bcl-w DNA fragment SEQ ID 37.  
XX  
KW Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;  
KW prion; inhibition; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100587-C1.  
XX  
PD 21-NOV-2002.  
XX  
PP 09-JAN-2001; 2001DE-1000587.  
XX  
PP 09-JAN-2001; 2001DE-1000587.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
XX WPI; 2002-742209/81.  
XX  
PT Inhibiting expression of target genes, e.g. oncogenes, in cells, by  
PT introduction of complementary double-stranded oligoribonucleotide,  
PT after treating the cell with interferon -  
XX  
PS Disclosure; Page 35-36; 98pp; German.  
XX  
CC This invention describes a novel method for inhibiting expression of a  
CC target gene by introducing into the cell that contains the target gene  
CC at least one oligoribonucleotide (dsRNAI) that has a double-stranded  
CC (ds) structure of not more than 49 consecutive nucleotides (nt), where  
CC at least a segment of one strand of the ds structure is complementary  
CC with the target gene and the cells are treated with interferon before  
CC introduction of dsRNAI. The method is used to inhibit expression of  
CC target genes, particularly oncogenes, cytokine genes, Id (not defined)  
CC protein genes; developmental or prion genes, or genes expressed in  
CC pathogenic organisms (particularly plasmodia) or in viruses or viroids  
CC (pathogenic in humans, animals or plants). Treating the cells with  
CC interferon greatly increases the extent to which dsRNA can inhibit  
CC expression of the target genes, and the effect is even greater when dsRNA  
CC are modified to increase their stability. ABX09936-ABX10075 represent  
CC gene fragments used to illustrate the method of the invention.  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;  
Query Match 99.8%; Score 582; DB 24; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.7e-135;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ATGGGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
Db 1 ATGGGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60  
QY 61 AAGCTGAGGCAGAGGGTTATGTCTGTGAGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGAGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCACC 180  
Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCACC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGCTGAGTTCAGCCAGCAACGCTTCACC 240  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGCTGAGTTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGCGCTTGTAGCCTTCTTT 300  
Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGCGCTTGTAGCCTTCTTT 300



XX WPI; 2002-270454/32.  
XX  
PT Inhibiting gene expression in cells, useful for e.g. treating tumors,  
PT by introducing double-stranded complementary oligoRNA having unpaired  
PT terminal bases -  
XX  
XX  
PS Claim 13; Page 32; 104pp; German.  
XX  
CC The invention relates to a method for inhibiting expression of a target  
CC gene (ABL91658-ABL91797) in a cell by introducing at least one  
CC oligoribonucleotide that has a double-stranded structure consisting of at  
CC most 49 sequential nucleotide pairs, with at least part of one strand  
CC complementary with the target gene and has at least one end a  
CC single-stranded segment of 1-4 nt. The method provides  
CC oligoribonucleotides for antisense inhibition of gene expression useful  
CC e.g. for treating tumors but the oligoribonucleotides may also be  
CC directed against genes present in pathogens (e.g. Plasmodium or  
CC viruses/viroids, pathogenic or humans, animals or plants) or against  
CC cytokine, id, developmental or prion genes. The method provides more  
CC effective inhibition of gene expression than use of known  
CC oligonucleotides, probably because the unpaired overhang increases  
CC stability and thus intracellular concentration.  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;  
  
Query Match 99.8%; Score 582; DB 24; Length 582;  
Best Local Similarity 100.0%; Pred. No. 3.7e-135;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60  
Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60  
  
Qy 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
  
Qy 121 CCGTGTACCAAGCCATGCGGGCAGCTGGAGATGAGTTCAGACCCGCTTCGGGGCACC 180  
Db 121 CCGTGTACCAAGCCATGCGGGCAGCTGGAGATGAGTTCAGACCCGCTTCGGGGCACC 180  
  
Qy 181 TTCTCTGATCTGGCGGCTCAGCTGATGTACCCAGGCTCAGCCAGCAACGCTTACC 240  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTACCCAGGCTCAGCCAGCAACGCTTACC 240  
  
Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGGCTTGTAGCCTTTT 300  
Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGGCTTGTAGCCTTTT 300  
  
Qy 301 GTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Db 301 GTCTTTGGGGCTGCACTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
  
Qy 361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
  
Qy 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGGCGGG 480  
Db 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGGCGGG 480  
  
Qy 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTCTACGGGGCGGCGCTGGCACTG 540  
Db 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTCTACGGGGCGGCGCTGGCACTG 540  
  
Qy 541 GGGGCCCTGTAACTGTAGGGGCCCTTTTGTAGCAAGTGA 582  
Db 541 GGGGCCCTGTAACTGTAGGGGCCCTTTTGTAGCAAGTGA 582

ID ABT16642 standard; DNA; 3542 BP.  
XX  
AC ABT16642;  
XX  
DT 03-APR-2003 (first entry)  
XX  
DE Human bcl-2 gene SEQ ID No 4.  
XX  
KW Anti-tumour; DNazyme; bcl-2 gene; tumour; malignant; chemotherapy;  
KW radiation therapy; catalytic domain; enzyme; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200299090-A1.  
XX  
PD 12-DEC-2002.  
XX  
PF 07-JUN-2002; 2002WO-AJ00739.  
XX  
PR 07-JUN-2001; 2001AU-0005527.  
XX  
PA (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.  
XX  
PI Sun J, Wang L, Turner RJ, Saravolac EG, Dass CR;  
XX  
DR WPI; 2003-140617/13.  
XX  
PT Novel DNazyme useful for treating tumors, and for enhancing the  
PT sensitivity of malignant or virus infected cells to therapy, comprises  
PT a catalytic domain and binding domain contiguous to the catalytic  
PT domain -  
XX  
PS Disclosure; Page 44-45; 67pp; English.  
XX  
CC The invention relates to a DNazyme which specifically cleaves mRNA  
CC transcribed from a member of the bcl-2 gene family. The DNazymes comprise  
CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
CC the catalytic domain, and therefore hybridise with, the two regions  
CC immediately flanking the purine residue of the cleavage site within the  
CC bcl-2 gene family mRNA, at which DNazyme-catalysed cleavage is desired. A  
CC pharmaceutical composition comprising a DNazyme of the invention is  
CC useful for treating tumours in a subject, and for enhancing the  
CC sensitivity of malignant or virus infected cells infected cells to  
CC therapy. The DNazymes are useful in diagnostics, therapeutics,  
CC prophylaxis, research agents and in kits. The DNazymes are also  
CC useful for increasing the susceptibility of tumour cells to anti-tumour  
CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
CC sequence represents a human bcl-2 gene of the invention.  
XX  
SQ Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 other;  
  
Query Match 99.5%; Score 579.8; DB 25; Length 3542;  
Best Local Similarity 99.7%; Pred. No. 2e-134;  
Matches 581; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 60  
Db 177 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 236  
  
Qy 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
Db 237 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 296  
  
Qy 121 CCGTGTACCAAGCCATGCGGGCAGCTGGAGATGAGTTCAGACCCGCTTCGGGGCACC 180  
Db 297 CCGTGTACCAAGCCATGCGGGCAGCTGGAGATGAGTTCAGACCCGCTTCGGGGCACC 356  
  
Qy 181 TTCTCTGATCTGGCGGCTCAGCTGATGTACCCAGGCTCAGCCAGCAACGCTTACC 240  
Db 357 TTCTCTGATCTGGCGGCTCAGCTGATGTACCCAGGCTCAGCCAGCAACGCTTACC 416  
  
Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGGCTTGTAGCCTTTT 300

Db 417 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAACCTGGGGCGCCCTTGTAGCCTTCCTT 476  
QY 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Db 477 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 536  
QY 361 CAAAGTGCAGGAGTGGATGGTGGCCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
Db 537 CAAAGTGCAGGAGTGGATGGTGGCCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596  
QY 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGACGCGGCGCCCTGGAGGAGCGCGG 480  
Db 597 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGACGCGGCGCCCTGGAGGAGCGCGG 656  
QY 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCGCGTGGCACTG 540  
Db 657 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCGCGTGGCACTG 716  
QY 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGAA 583  
Db 717 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGAA 759

RESULT 6  
AAT96577  
ID AAT96577 standard; DNA; 583 BP.  
XX  
AC AAT96577;  
XX  
DT 22-APR-1998 (first entry)  
XX Human bcl-w DNA.  
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
KW diagnosis; degenerative disease; ss.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH 1..582  
FT CDS /\*tag= a  
FT /product= bcl-w

XX W09735971-A1.  
XX  
PD 02-OCT-1997.  
XX  
PF 27-MAR-1997; 97WO-AU00199.  
XX  
PR 27-MAR-1996; 96AU-0008965.  
XX (AMPA-) AYRAD OPERATIONS PTY LTD.  
PA  
XX Adams JM, Cory S, Gibson LM, Holmgreen SP;  
XX  
XX WPI; 1997-489635/45.  
DR P-PSDB; AAW36047.  
XX  
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
PT or inhibit cell survival, e.g. for treatment of cancer and  
PT degenerative diseases  
XX  
PS Claim 3; Page 48; 86pp; English.  
XX

CC This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene  
CC family, extracted from an adult brain library. This gene promotes cell  
CC survival, so its modulation is useful in treatment of cancer or  
CC auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's  
CC disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,  
CC human immunodeficiency virus infection or in cell transplants.  
CC Up-regulation of the gene can also be used to modify cell lines cultured  
CC in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas  
CC and to increase survival of primary explants during genetic modification.

CC It can be used to produce recombinant Bcl-w for therapy, diagnosis,  
CC antibody production or screening of potential modulators.  
XX  
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;  
Query Match 99.2%; Score 578.2; DB 18; Length 583;  
Best Local Similarity 99.5%; Pred. No. 3.3e-134;  
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCCGACGCTCGGCCCCAGACACACGCGGCTCTGTGGCAGACTTTGTAGCTTAT 60  
Db 1 ATGGCGACCCCGACGCTCGGCCCCAGACACACGCGGCTCTGTGGCAGACTTTGTAGCTTAT 60  
QY 61 AAGCTGAGGCAGAAGGGTTATGTCTGTGAGAGTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
Db 61 AAGCTGAGGCAGAAGGGTTATGTCTGTGAGAGTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCAC 180  
Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGCGCAC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGTCTCCGAGAACTTTTCAAGGGGCCCCAACTGGGCGCGCTTGTAGCCTTCCTT 300  
Db 241 CAGGTCTCCGAGAACTTTTCAAGGGGCCCCAACTGGGCGCGCTTGTAGCCTTCCTT 300  
QY 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Db 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
QY 361 CAAAGTGCAGGAGTGGTGGCCCTACCTGGAGACGCGGCTGGTGCATGCCATCCACAGC 420  
Db 361 CAAAGTGCAGGAGTGGTGGCCCTACCTGGAGACGCGGCTGGTGCATGCCATCCACAGC 420  
QY 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGCGCTGGAGGAGGCGCGG 480  
Db 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGCGCTGGAGGAGGCGCGG 480  
QY 481 CGTCTCGGGAGGGAACTGGGCAATCAGTGAGGACAGTGTGACGGGGCGCTGGCACTG 540  
Db 481 CGTCTCGGGAGGGAACTGGGCAATCAGTGAGGACAGTGTGACGGGGCGCTGGCACTG 540  
QY 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGAA 583  
Db 541 GGGGCCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGAA 583

RESULT 7  
AAX25134  
ID AAX25134 standard; DNA; 583 BP.  
XX  
AC AAX25134;  
XX  
DT 05-JUL-1999 (first entry)  
XX Human bcl-w gene derivative.  
XX  
XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
XX animal model; ss.  
XX Homo sapiens.  
XX  
PN W09913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU00764.  
XX  
PR 16-SEP-1997; 97AU-0009228.  
XX



PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;  
PI WPI; 1999-243890/20.  
XX P-PSDB; AAY05532.  
DR An animal model exhibiting reduced levels of a Bcl-w protein and/or  
XX protein associated with Bcl-w  
PS Disclosure; Page 36; 52pp; English.  
XX  
XX The present sequence is described as a derivative of the human  
CC bcl-w gene (see AAX25132) and encodes Bcl-w protein (see AAY05532), a  
CC pro-survival member of the Bcl-2 family which is widely expressed  
CC and which is essential for spermatogenesis. The invention relates  
CC generally to a method of treatment and to an animal model for the  
CC identification of molecules and genetic sequences useful for  
CC inducing or reducing fertility of male animals. Methods are  
CC provided for the treatment of infertility, or for reducing  
CC fertility, by modulating spermatogenesis. An animal model carries  
CC a mutation is at least one allele of the human or murine bcl-w gene  
CC or in a gene associated with bcl-w. Such animals have disorganised  
CC seminiferous tubules and are substantially infertile, but possess no  
CC other major abnormalities as determined by histological examination.  
CC They can be used to screen for therapeutic molecules including  
CC genetic sequences capable of inducing, enhancing or otherwise  
CC facilitating spermatogenesis in animals, or which can induce  
CC infertility.  
XX  
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;  
  
Query Match 99.2%; Score 578.2; DB 20; Length 583;  
Best Local Similarity 99.5%; Pred. No. 3.3e-134;  
Matches 580; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 ATGGGACCCCGCTCGGCCCGGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Db |||||  
QY 61 AAGCTGAGGACGAAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
Db |||||  
QY 121 CCGTGCACCAAGCCCATGCGGCGAGCTGAGTTCGAGACCCGCTTCGGGCGCACC 180  
Db |||||  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGGCTCAGCCAGCAACGCTTCACC 240  
Db |||||  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCGCCCAACTGGGCGCGCTTGTAGCCTTCCTT 300  
Db |||||  
QY 301 GTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360  
Db CTCTTTGGGGCTGCACTGTGTGTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360  
QY 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
Db |||||  
QY 421 AGTGGGGCTGGGCGAGTTTCACAGCTCTATACGGGGACGGGCGCCTGGAGGAGGCGCGG 480  
Db |||||  
QY 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTCTAGCGGGCGCCGTGGCACTG 540  
Db CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTCTAGCGGGCGCCGTGGCACTG 540  
QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGCTAGCAAGTGAA 583

Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGCTAGCAAGTGAA 583  
  
RESULT 8  
AAX25132  
ID AAX25132 standard; DNA; 581 BP.  
XX AAX25132;  
AC AAX25132;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human bcl-w gene.  
XX Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
KW animal model; ss.  
XX Homo sapiens.  
OS  
XX MO9913710-A1.  
PN 25-MAR-1999.  
PD 16-SEP-1998; 98WO-AU00764.  
PF 16-SEP-1997; 97AU-0009228.  
PR (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
XX Adams J, Cory S, Gibson L, Koentgen F, Print C;  
PI WPI; 1999-243890/20.  
DR P-PSDB; AAY05530.  
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w  
XX Claim 3; Page 32; 52pp; English.  
XX  
CC The present sequence is the human bcl-w gene encoding Bcl-w protein  
CC (see AAY05530), a pro-survival member of the Bcl-2 family which is  
CC widely expressed and which is essential for spermatogenesis. The  
CC invention relates generally to a method of treatment and to an  
CC animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male  
CC animals. Methods are provided for the treatment of infertility, or  
CC for reducing fertility, by modulating spermatogenesis. An animal  
CC model carries a mutation is at least one allele of the human or  
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals  
CC have disorganised seminiferous tubules and are substantially  
CC infertile, but possess no other major abnormalities as determined  
CC by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of  
CC inducing, enhancing or otherwise facilitating spermatogenesis in  
CC animals, or which can induce infertility.  
XX  
SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;  
  
Query Match 99.1%; Score 577.8; DB 20; Length 581;  
Best Local Similarity 99.7%; Pred. No. 4.1e-134;  
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
  
QY 1 ATGGCGACCCCGCTCGGCCCGGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Db |||||  
QY 61 AAGCTGAGGACGAAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
Db |||||  
QY 121 CCGTGCACCAAGCCCATGCGGCGAGCTGAGTTCGAGACCCGCTTCGGGCGCACC 180  
Db |||||

QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
|||  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCAAACGCTTCACC 240  
  
QY 241 CAGGTCTCCAGCAACTTTTCAAGGGGGCCCCAACTGGGGCGCCTTGTAGCCTTCTTT 300  
|||  
Db 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGCGCCTTGTAGCCTTCTTT 300  
  
QY 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
|||  
Db 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
  
QY 361 CAAGTGCAGGAGTGATGGTGGCTACCTGGAGACGCGGCTGCTGACTGGATCCACAGC 420  
|||  
Db 361 CAAGTGCAGGAGTGATGGTGGCTACCTGGAGACGCGGCTGCTGACTGGATCCACAGC 420  
  
QY 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGCGCCTGGAGGAGCGCGG 480  
|||  
Db 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGCGCCTGGAGGAGCGCGG 480  
  
QY 481 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCGCTGSCACTG 540  
|||  
Db 481 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCGCTGSCACTG 540  
  
QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTCTAGCAAGTG 581  
|||  
Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTCTAGCAAGTG 581

RESULT 9  
AAV28334  
ID AAV28334 standard; cDNA; 579 BP.  
XX  
AC AAV28334;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Human bcl-y gene.  
XX  
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
XX  
KW Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..579  
FT /\*tag= a  
FT /product= bcl-y  
FT /note= "No stop codon given"

XX US5789201-A.  
XX  
PD 04-AUG-1998.  
XX  
PF 11-FEB-1997; 97US-0798897.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastella J;  
XX  
DR WPI; 1998-446079/38.  
DR P-PSDB; AAW61392.  
XX  
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for  
PT producing recombinant protein for use in treating uncontrolled cell  
PT growth e.g. cancers  
XX  
PS Claim 3; Column 15/16; 27pp; English.  
XX  
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2

CC family, components in the cell death pathway. The bcl-2 family  
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y  
CC falls in the apoptosis activity category. The recombinant protein may  
CC be used to prevent uncontrolled cell growth, either by its direct  
CC administration to recombinant genetic constructs to increase its  
CC expression in vivo. Also, antisense constructs can be used in disorders  
CC where prevention of cell death is desired.  
XX  
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 19; Length 579;  
Best Local Similarity 99.3%; Pred. No. 8.1e-133;  
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
|||  
Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
  
QY 61 AAGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
|||  
Db 61 AAGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCGCTTCGGCGCAC 180  
|||  
Db 121 CCACTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCGCTTCGGCGCAC 180  
  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 240  
|||  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 240  
  
QY 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGCGCCTTGTAGCCTTCTTT 300  
|||  
Db 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGCGCCTTGTAGCCTTCTTT 300  
  
QY 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
|||  
Db 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
  
QY 361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
|||  
Db 361 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
  
QY 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGCGCCTGGAGGAGCGCGG 480  
|||  
Db 421 AGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGACGGGCGCCTGGAGGAGCGCGG 480  
  
QY 481 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGCAGCTG 540  
|||  
Db 481 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGCAGCTG 540  
  
QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTCTAGCAAG 579  
|||  
Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTCTAGCAAG 579

RESULT 10  
AAV15946  
ID AAV15946 standard; cDNA; 579 BP.  
XX  
AC AAV15946;  
XX  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE cDNA encoding the human bcl-y protein.  
XX

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite; ss.

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XX Homo sapiens.
CS
XX
PN US5883229-A.
XX
PD 16-MAR-1999.
XX
PF 25-NOV-1997; 97US-0978523.
XX
PR 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
PR 25-NOV-1997; 97US-0978523.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1999-214150/18.
DR P-PSDB; AAW97392.
XX
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful
PT for modulating programmed cell death
XX
PS Disclosure; Columns 15-16; 26pp; English.
XX
CC The present sequence encodes human bcl-y protein (Hbcl-y). The
CC specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y
CC proteins may be used to treat conditions associated with a disruption of
CC the cell death pathway. If they act as cell death inhibitors, they may be
CC used in therapies to treat subjects suffering from: strokes, head trauma,
CC Alzheimer's Disease, neural and muscular degenerative diseases
CC (especially multiple sclerosis), myocardial infarction, vitally induced
CC cell death, aging, spinal cord injuries and amyotrophic lateral
CC sclerosis- conditions where cells under go premature cell death as a
CC result of triggers which may or may not be apparent. They may also be
CC used in this way to develop cell lines which remain viable in culture for
CC an extended period. In contrast, if they act as cell death stimulators,
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and
CC lung cancer) and auto/hyperimmune diseases. They may also be used to
CC cause cell death in, and hence controil, parasites.
XX
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 98.2%; Score 572.6; DB 20; Length 579;
Best Local Similarity 99.3%; Pred. No. 8.1e-133;
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGACCTCGGCCCGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
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QY 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAGGAGATGGAACCACTGGTGGGA 360
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DT 02-OCT-1998 (first entry)
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DE Rat bcl-y gene.
XX
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.
XX
OS Rattus sp.
XX
FH Key Location/Qualifiers
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FT /*tag= a
FT /product= bcl-y
FT /note= "No stop codon given"
XX
PN US5789201-A.
XX
PD 04-AUG-1998.
XX
PF 11-FEB-1997; 97JS-0798897.
XX
PR 23-FEB-1996; 96US-0012201.
PR 11-FEB-1997; 97US-0798897.
XX
PA (COCE-) COCENSYS INC.
XX
PI Guastella J;
XX
DR WPI; 1998-446079/38.
DR P-PSDB; AAW61391.
XX
PT Nucleic acids encoding B-cell lymphoma-y protein - useful for
PT producing recombinant protein for use in treating uncontroilled cell
PT growth e.g. cancers
XX
PS Claim 2; Column 13/14; 27pp; English.
XX
CC The mammalian bcl-y genes encode a protein that is a member of the bcl-2
CC family, components in the cell death pathway. The bcl-2 family
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y
CC falls in the apoptosis activity category. The recombinant protein may
CC be used to prevent uncontroilled cell growth, either by its direct
CC administration to recombinant genetic constructs to increase its
CC expression in vivo. Also, antisense constructs can be used in disorders
CC where prevention of cell death is desired.
XX
SQ Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

Query Match 90.5%; Score 527.8; DB 19; Length 579;
Best Local Similarity 94.5%; Pred. No. 1.1e-121;
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Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

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|||  
Db 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
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QY 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCAGCAGCTGAC 120  
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QY 121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 180  
|||  
Db 121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCGGGCGCAC 180  
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Db 181 TTCTCTGACCTGGCGCTCAGCTACACGTGACCCCGAGGCTCAGCCAGCAACGCTTCACC 240  
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QY 241 CAGGTCTCCGACGAACTTTTCAAGSGGGCCCCAACTGGGGCGCCCTTTAGCCTTCCTT 300  
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RESULT 12  
AAX15945  
ID AAX15945 standard; cDNA; 579 BP.  
XX  
AC AAX15945;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE cDNA encoding the rat bcl-y protein.

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite; ss.  
XX  
OS Rattus sp.  
XX  
PN US5883229-A.  
XX  
PD 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-0978523.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
PR 25-NOV-1997; 97US-0978523.

(COCE-) COCENSYS INC.  
Guastella J;  
WPI; 1999-214150/18.  
P-PSDB; AAW97391.  
Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
for modulating programmed cell death  
Disclosure; Columns 13-16; 26pp; English.  
The present sequence encodes rat bcl-y protein (Rbcl-y). The  
specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
proteins may be used to treat conditions associated with a disruption of  
the cell death pathway. If they act as cell death inhibitors, they may be  
used in therapies to treat subjects suffering from: strokes, head trauma,  
Alzheimer's Disease, neural and muscular degenerative diseases  
(especially multiple sclerosis), myocardial infarction, vitally induced  
cell death, aging, spinal cord injuries and amyotrophic lateral  
sclerosis- conditions where cells under go premature cell death as a  
result of triggers which may or may not be apparent. They may also be  
used in this way to develop cell lines which remain viable in culture for  
an extended period. In contrast, if they act as cell death stimulators,  
Rbcl-y and Hbcl-y may be used to treat conditions associated with  
prolonged cell life span such as cancer (especially kaposi's sarcoma and  
lung cancer) and auto/hyperimmune diseases. They may also be used to  
cause cell death in, and hence control, parasites.  
Sequence 579 BP; 111 A; 157 C; 198 G; 113 T; 0 other;

Query Match 90.5%; Score 527.8; DB 20; Length 579;  
Best Local Similarity 94.5%; Pred. No. 1.1e-121;  
Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
|||  
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GenCore version 5.1.6  
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and is derived by analysis of the total score distribution.

SUMMARIES

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1	572.6	98.2	579	1 US-08-798-897-2	Sequence 2, Appli
2	572.6	98.2	579	2 US-08-978-523-2	Sequence 2, Appli
3	527.8	90.5	579	1 US-08-798-897-1	Sequence 1, Appli
4	527.8	90.5	579	2 US-08-978-523-1	Sequence 1, Appli
5	428.4	73.5	1864	4 US-09-149-476-130	Sequence 130, App
6	131	22.5	926	1 US-08-081-448-5	Sequence 5, Appli
7	131	22.5	926	2 US-08-470-670A-6	Sequence 6, Appli
8	131	22.5	926	3 US-08-481-739-1	Sequence 1, Appli
9	131	22.5	926	3 US-09-167-921-1	Sequence 1, Appli
10	131	22.5	926	3 US-09-277-020-39	Sequence 39, Appli
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12	131	22.5	926	4 US-08-461-511A-6	Sequence 6, Appli
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18	123.4	21.2	5086	2 US-08-465-485A-19	Sequence 19, Appli
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43	70	12.0	623	6 5506344-3	Patent No. 5506344
44	52.6	9.0	737	1 US-08-081-448-7	Sequence 7, Appli
45	52.6	9.0	737	2 US-08-470-670A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-08-798-897-2  
; Sequence 2, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
; US-08-798-897-2

Query Match 98.2%; Score 572.6; DB 1; Length 579;  
Best Local Similarity 99.3%; Pred. No. 8.3e-140;  
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
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Db 61 AAGCTGAGGACAGAGGTTATGCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
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Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCCAACTGGGGCCGCTTGTAGCCTTCTT 300  
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Qy 361 CAAGTGCAGGAGTGGATGCTGGCCCTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420  
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Db 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579

RESULT 2  
US-08-978-523-2  
; Sequence 2, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.C, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-08-978-523-2  
  
Query Match 98.2%; Score 572.6; DB 2; Length 579;  
Best Local Similarity 99.3%; Pred. No. 8.3e-140;  
Matches 575; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
  
Qy 1 ATGGCGACCCCGAGCTCGGGCCCCCAGACACACCGGCTCTGGTGGCAGACTTTGTAGTTAT 60  
Db 1 ATGGCGACCCCGAGCTCGGGCCCCCAGACACACCGGCTCTGGTGGCAGACTTTGTAGTTAT 60  
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Db 61 AAGCTGAGGACAGAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGGCCAGCAGCTGAC 120  
Qy 121 CCGCTGCACCAAGCCATCGCGGCAGCTGCATGTACCCAGGCTCAGCCCAAGCAGCTTCACC 180  
Db 121 CCGCTGCACCAAGCCATCGCGGCAGCTGCATGTACCCAGGCTCAGCCCAAGCAGCTTCACC 180  
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Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTACCCAGGCTCAGCCCAAGCAGCTTCACC 240  
Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCCAACTGGGGCCGCTTGTAGCCTTCTT 300  
Db 241 CAGGTCTCCGATGAACCTTTTCAAGGGGCCCCCAACTGGGGCCGCTTGTAGCCTTCTT 300  
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Db 301 GTCTTTGGGGCTGCACCTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Qy 361 CAAGTGCAGGAGTGGATGCTGGCCCTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGAGTGGATGCTGGCCCTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420  
Qy 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCTGGAGGAGGCGCGG 480  
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Qy 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGTGGCACTG 540  
Qy 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579  
Db 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579

RESULT 3  
US-08-798-897-1  
; Sequence 1, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn: Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-08-798-897-1

Query Match 90.5%; Score 527.8; DB 2; Length 579;  
Best Local Similarity 94.5%; Pred. No. 3.6e-128;  
Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 1 ATGGGACCCAGCCCTGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Db 1 ATGGGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGTTAT 60  
QY 61 AAGCTGAGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
Db 61 AAGCTGAGACAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCAGCC 180  
Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCGGGGCAGCC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGGCTCAGCCAGCAACGCTTACCC 240  
Db 181 TTCTCTGACCTGGCGGCTCAGCTGCATGTGACCCCGAGGCTCAGCCAGCAACGCTTACCC 240  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300  
Db 241 CAGGTTTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTGGCATTCTTT 300  
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Db 301 GTCTTTGGGGTGCCTGTGTCTGAGAGTGTCAACAAGAAATGGAGCCATTGGTGGGA 360  
QY 361 CAAGTGCAGAGTGGATGGTGGCTTACCTGGAGACGGGGCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGATGGATGGTGGCTTACCTGGAGACACGCTTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGGG 480  
Db 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGG 480  
QY 481 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGGCACTG 540  
Db 481 CGTCTGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGGCACTG 540  
QY 541 GGGGCCCTGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAG 579  
Db 541 GGGGCCCTGTAACTGTAGGGGCCCTTTTGTGCTAGCAAG 579

RESULT 4  
US-08-978-523-1  
Sequence 1, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-08-978-523-1

Query Match 90.5%; Score 527.8; DB 2; Length 579;  
Best Local Similarity 94.5%; Pred. No. 3.6e-128;  
Matches 547; Conservative 0; Mismatches 32; Indels 0; Gaps 0;  
QY 1 ATGGGACCCAGCCCTGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Db 1 ATGGGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGTTAT 60  
QY 61 AAGCTGAGGACAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
Db 61 AAGCTGAGACAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCCAGCAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCAGCC 180  
Db 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTCGGGGCAGCC 180  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGGCTCAGCCAGCAACGCTTACCC 240  
Db 181 TTCTCTGACCTGGCGGCTCAGCTGCATGTGACCCCGAGGCTCAGCCAGCAACGCTTACCC 240  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300  
Db 241 CAGGTTTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTGGCATTCTTT 300  
QY 301 GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Db 301 GTCTTTGGGGTGCCTGTGTCTGAGAGTGTCAACAAGAAATGGAGCCATTGGTGGGA 360  
QY 361 CAAGTGCAGGATGGATGGTGGCCCTACTTGAGACGGGGCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGATGGATGGTGGCCCTACTTGAGACACGCTTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGGG 480  
Db 421 AGTGGGGCTGGGGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCGG 480

QY 481 CGTCTGCGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCGGTGGCACTG 540  
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D5 481 CGTCTGCGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCGGTGGCACTG 540  
QY 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579  
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D5 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579

RESULT 5

US-09-149-476-130  
; Sequence 130, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,626  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,334  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,336  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,163  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/047,600  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,598  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596

; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER FILING DATE: 1997-04-11  
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; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
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; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
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; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER FILING DATE: 1997-08-22  
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; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/056,910  
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; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
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EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
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EARLIER APPLICATION NUMBER: 60/047,589  
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EARLIER APPLICATION NUMBER: 60/047,593  
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EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 73.5%; Score 428.4; DB 4; Length 1864;  
Best Local Similarity 99.3%; Pred. No. 3.3e-102;  
Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTAT 60  
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Db 11 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTAT 70  
QY 61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCGCAGCAGTGC 120  
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Db 71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCGCAGCAGTGC 130  
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Db 131 CCGCTGCACCAAGCCATCGGGCAGCKGGAGATGAGTTCGAGACCCCGCTTCGGCGCACC 190  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCGCAGCAACGCTTCACC 240  
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Db 191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCGCAGCAACGCTTCACC 250  
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Db 311 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAAACCACTGTGGGA 370  
QY 361 CAAGTCAGGAGTGGATGCTGCCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420  
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Db 371 CAAGTCAGGAGTGGATGCTGCCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 430  
QY 421 AGTGGGGCTGG 432  
Db 431 AGTGGGGCTGG 442

RESULT 6

US-08-081-448-5  
; Sequence 5, Application US/08081448  
; Patent No. 5646008  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Boise, Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5646008th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,448  
; FILING DATE: 19930622  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5646008thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-744-0090  
; TELEFAX: 312-755-4489  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS







US-09-277-020-39

Query Match 22.5%; Score 131; DB 3; Length 926;  
Best Local Similarity 56.3%; Pred. No. 4.5e-25;  
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

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Db 364 CCCGGAGGTGATCCCATGGCAGCAGTAACCAAGCGCTGAGGGAGCGAGCGAGT 423
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 158 TCGAGACCCGCTTCGGCGCACCTTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAG 217
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Db 424 TTGAAGTGGGTACCGCGGCGCATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483
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QY 218 GCTCAGACCCGCTTCGGCGCACCTTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAG 217
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Db 484 TTGAAGTGGGTACCGCGGCGCATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483
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QY 278 GGGGGCCGCTTGTAGCCTTTTGTCTTTTGGGCTGCACCTGCTGCTGAGAGTGTCAACA 337
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Db 544 GGGGTGCGATTGTGGCCTTTTCTCCTTCGGCGGGCACCTGTGCGTGGAAAGCGTAGACA 603
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QY 338 AGGAGATGGAACCACTGGTGGGACAAGTGCAGAGTGGATGGTGGCCTACCTGGAGACGC 397
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Db 604 AGGAGATGCGAGTATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 663
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QY 398 GGCTGGCTGACTGGATCCACAGCAGTGGGGCTGGGCGGAGTTTCACAGCTCTATACGGGG 457
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Db 664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGGGAACCTCTATGGGA 723
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QY 458 ACGGGCCCTGGAGGAGCGCGGCGCTCTCGCGAGGGGAACCTGGGCTCAGTGAGGACAG 517
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Db 724 ACAATGCAGCAGCCGAGAGCCGAAGGGCCAGGAACGCTTCAACCGCTGGTTCTTGACGG 783
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QY 518 TGCTGACGGGGCGCG 532
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RESULT 11

US-09-323-743-1  
; Sequence 1, Application US/09323743  
; Patent No. 6214986  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0368  
; CURRENT APPLICATION NUMBER: US/09/323,743  
; CURRENT FILING DATE: 1999-06-01  
; EARLIER APPLICATION NUMBER: 09/277,020  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 09/167,921  
; EARLIER FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(836)  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: L20121 Genbank  
; DATABASE ENTRY DATE: 1994-07-26

Query Match 22.5%; Score 131; DB 3; Length 926;  
Best Local Similarity 56.3%; Pred. No. 4.5e-25;

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Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;
QY 98 CCGGGAGGGCCCGCAGCTGACCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGT 157
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Db 364 CCCGGAGGTGATCCCATGGCAGCAGTAACCAAGCGCTGAGGGAGCGAGCGAGT 423
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QY 158 TCGAGACCCGCTTCGGCGCACCTTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAG 217
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Db 424 TTGAAGTGGGTACCGCGGCGCATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483
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QY 218 GCTCAGACCCGCTTCGGCGCACCTTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAG 217
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Db 484 TTGAAGTGGGTACCGCGGCGCATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483
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QY 278 GGGGGCCGCTTGTAGCCTTTTGTCTTTTGGGCTGCACCTGCTGCTGAGAGTGTCAACA 337
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Db 544 GGGGTGCGATTGTGGCCTTTTCTCCTTCGGCGGGCACCTGTGCGTGGAAAGCGTAGACA 603
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QY 338 AGGAGATGGAACCACTGGTGGGACAAGTGCAGAGTGGATGGTGGCCTACCTGGAGACGC 397
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Db 604 AGGAGATGCGAGTATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 663
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QY 398 GGCTGGCTGACTGGATCCACAGCAGTGGGGCTGGGCGGAGTTTCACAGCTCTATACGGGG 457
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Db 664 ACCTAGAGCCTTGGATCCAGGAGAACGGCGGCTGGGATACTTTTGGGAACCTCTATGGGA 723
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QY 458 ACGGGCCCTGGAGGAGCGCGGCGCTCTCGCGAGGGGAACCTGGGCTCAGTGAGGACAG 517
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Db 724 ACAATGCAGCAGCCGAGAGCCGAAGGGCCAGGAACGCTTCAACCGCTGGTTCTTGACGG 783
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QY 518 TGCTGACGGGGCGCG 532
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Db 784 GCATGACTGTGGCGG 798
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RESULT 12

US-08-461-511A-6  
; Sequence 6, Application US/08461511A  
; Patent No. 6303331  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.B.  
; Boise, Lawrence H.  
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS  
; AND METHODS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,511A  
; FILING DATE: 05-Jun-1995  
; CLASSIFICATION: UNKNOWN  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARCD:179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single





PCT-US94-07089-6

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Query Match          22.5%; Score 131; DB 5; Length 926;
Best Local Similarity 56.3%; Pred. No. 4.5e-25;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGCCCCAGCAGCTGACCGCTGACCAAGCCATCGGGCAGCTGAGATGAGT 157
Db 364 CCGGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTAGGGAGGCGGACGAGT 423

QY 158 TCGAGACCCGCTTCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAG 217
Db 424 TTGAAGTGGGTACCGCGGCATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 483

QY 218 GCTCAGCCCAACAGCTTCAACCAGGTCTCCGACGAACTTTTCAAGGGGCCCAACT 277
Db 484 GGCAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACTCTTCGGGATGGGTAACT 543

QY 278 GGGCGCGCTTGTAGCCTTCTTGTCTTTGGGGCTGGCACTGTGCTGAGAGTGTCAACA 337
Db 544 GGGTGGCATTTGGCCCTTTTCTCCTTCGGCGGGGCACTGTGCGTGGAAAGCGTAGACA 603

QY 338 AGGAGATGGAACCACTGGTGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGC 397
Db 604 AGGAGATGCAGGTATTGGTGAATCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 663

QY 398 GGTGGCTGACTGGATCCACAGAGTGGGGCTGGCGGAGTTACAGCTCTATACGGGG 457
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QY 458 ACGGGCCCTGGAGGAGCGCGGCTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAG 517
Db 724 ACAATGAGCAGCCGAGAGCCGAAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 783

QY 518 TGCTGACGGGGCCG 532
Db 784 GCATGACTGTGGCCG 798
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RESULT 15

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US-08-465-485A-20
Sequence 20, Application US/08465485A
Patent No. 5831066
GENERAL INFORMATION:
APPLICANT: Reed, John
TITLE OF INVENTION: Regulation of bcl-2 Gene Expression
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 S. Jefferson Davis Hwy., Suite 400
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,485A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/124,256
FILING DATE: 20-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,716
FILING DATE: 21-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/288,692
FILING DATE: 22-DEC-1988
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; ATTORNEY/AGENT INFORMATION:
; NAME: Fortney, Andrew D.
; REGISTRATION NUMBER: 34,600
; REFERENCE/DOCKET NUMBER: 3335-070-55 CONT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (408) 436-2070
; TELEFAX: (408) 436-2075
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 717 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..717
; US-08-465-485A-20
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Query Match          21.2%; Score 123.4; DB 2; Length 717;
Best Local Similarity 58.6%; Pred. No. 4e-23;
Matches 214; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

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Db 244 GCGGGCCTGCGCTCAGCCCGGTGCCACCTGTGGTCCACCTGGCCCTCCGCCAAGCCGCG 303

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QY 211 ACCCAGGCTCAGCCCCAGCAACGTTTACCCAGGTCTCCGACGAACTTTTCAAGGGGCG 270
Db 364 AGCCCTTCACCGCGGGGACGCTTTGCCACGGTGTGGAGAGCTCTTCAGGGACGGG 423

QY 271 CCCAACTGGGCGCGCCTTGTAGCCTTCTTTGTCTTTGGGCTGCACCTGTGTGCTGAGAGT 330
Db 424 GTGAACTGGGGGAGGATTTGTGGCCTTCTTTGAGTTCGGTGGGTCTATGTGTGTGGAGAGC 483

QY 331 GTCAACAAGGAGATGGAACCACTGGTGGGACAAGTGCAGAGTGGATGGTGGCCTACCTG 390
Db 484 GTCAACCGGAGATGTGCCCCCTGGTGGACAACATCGCCCTGTGGATGACTGAGTACCTG 543

QY 391 GAGACGCGCTGGCTGACTGGATCCACAGCAGTGGGGCTGGCGGAGTTTCACAGCTCTA 450
Db 544 AACCGGCACCTGCACACCTGGATCCAGGATAACGGAGGCTGGGATGCCCTTTGTGGAAC 603

QY 451 TACGG 455
Db 604 TACGG 608
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GenCore version: 5.1.6  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(without alignments)  
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Title: US-09-925-674A-6  
Perfect score: 583  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

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Database : Published Applications NA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	583	100.0	583	10	US-09-925-674A-6	Sequence 6, Appli
2	524.4	89.9	582	10	US-09-925-674A-8	Sequence 8, Appli
3	428.4	73.5	1864	11	US-09-809-391-130	Sequence 130, App
4	428.4	73.5	1864	12	US-09-882-171-130	Sequence 130, App
5	428.2	73.4	578	12	US-10-029-386-10549	Sequence 10549, A
6	427.2	73.3	433	12	US-10-029-386-24249	Sequence 24249, A
7	257	44.1	6049	12	US-10-311-455-201	Sequence 201, App
8	223	38.3	6049	12	US-10-311-455-202	Sequence 202, App
9	152	26.1	590	12	US-10-029-386-13384	Sequence 13384, A
10	151	25.9	151	12	US-10-029-386-27084	Sequence 27084, A
11	150	25.7	150	9	US-09-864-761-17690	Sequence 17690, A
12	131	22.5	636	12	US-10-169-223-13	Sequence 13, Appli
13	131	22.5	702	11	US-09-959-987-9	Sequence 9, Appli
14	131	22.5	926	9	US-09-734-846-1	Sequence 1, Appli
15	131	22.5	926	9	US-09-734-847A-39	Sequence 39, Appli
16	131	22.5	926	10	US-09-952-278-5	Sequence 5, Appli

17	131	22.5	926	12	US-10-302-262-1	Sequence 1, Appli
18	131	22.5	926	14	US-10-072-830-3	Sequence 3, Appli
19	123.4	21.2	717	12	US-10-053-645A-20	Sequence 20, Appli
20	123.4	21.2	5086	8	US-08-726-211-4	Sequence 4, Appli
21	123.4	21.2	5086	12	US-10-141-618-11	Sequence 11, Appli
c 22	123.2	21.1	600	9	US-09-864-761-7360	Sequence 7360, Ap
c 23	122.2	21.0	555	9	US-09-864-761-24081	Sequence 24081, A
c 24	122.2	21.0	564	12	US-10-029-386-20790	Sequence 20790, A
25	121.8	20.9	1050	14	US-10-072-830-1	Sequence 1, Appli
26	121.8	20.9	6030	12	US-10-007-926A-117	Sequence 117, App
27	121.8	20.9	6030	14	US-10-171-581-187	Sequence 187, App
28	121.8	20.9	6142	14	US-10-198-846-13703	Sequence 13703, A
29	121	20.8	492	11	US-09-918-995-33305	Sequence 33305, A
30	120.4	20.7	1384	14	US-10-208-155-1	Sequence 1, Appli
31	119	20.4	615	12	US-10-053-645A-22	Sequence 22, Appli
32	119	20.4	911	8	US-08-726-211-6	Sequence 6, Appli
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34	96	16.5	439	9	US-09-864-761-912	Sequence 912, App
35	75.8	13.0	6509	12	US-10-311-455-199	Sequence 199, App
36	60.2	10.3	65	12	US-09-908-975-2435	Sequence 2435, Ap
37	52.6	9.0	737	10	US-09-952-278-7	Sequence 7, Appli
38	52.2	9.0	65	12	US-09-908-975-28692	Sequence 28692, A
39	50.8	8.7	432	10	US-09-917-800A-1467	Sequence 1467, Ap
40	50.6	8.7	657	12	US-09-908-147-3	Sequence 3, Appli
41	50.2	8.6	573	14	US-10-196-793A-45	Sequence 45, App
42	50.2	8.6	579	12	US-09-908-147-10	Sequence 10, Appli
43	50.2	8.6	579	12	US-09-908-147-18	Sequence 18, Appli
44	50.2	8.6	579	12	US-10-306-878-4	Sequence 4, Appli
45	50.2	8.6	624	14	US-10-277-693A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1

US-09-925-674A-6  
; Sequence 6, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-925-674A-6

Query Match 100.0%; Score 583; DB 10; Length 583;

Best Local Similarity 100.0%; Pred. No. 1.9e-150;  
Matches 583; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	61	AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGCCAGCAGCTGAC	120
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Qy 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420
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Qy 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 480
Db 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 480
Qy 481 CGTCTCGGGAGGGAACTGGGCACTCAGTGAGGACAGTCTGACGGGGCCGCTGGCACTG 540
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Qy 541 GGGGCCCTGGTAACCTGAGGGCCCTTTTGTGCTAGCAAGTGAA 583
Db 541 GGGGCCCTGGTAACCTGAGGGCCCTTTTGTGCTAGCAAGTGAA 583
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RESULT 2

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US-09-925-674A-8
; Sequence 8, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(579)
US-09-925-674A-8
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Query Match 89.9%; Score 524.4; DB 10; Length 582;
Best Local Similarity 93.8%; Pred. No. 2.3e-134;
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
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```
Qy 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
Db 1 ATGGCGACCCAGCCCTCAACCCCAACACACACGGGCTCTAGTGGTGA 60
Qy 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
Db 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGAAAGGCCAGCCGCGAC 120
Qy 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCCACC 180
Db 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGGAGACCCGCTTCGGGGCCACC 180
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```
Qy 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAGCAACGCTTCACC 240
Db 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCCAAGGCTCAGCCCAGCAACGCTTCACC 240
Qy 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300
Db 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTGGCAATCTTT 300
Qy 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360
Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTGGTGGGA 360
Qy 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGCCCTGGAGGAGGCGCGG 480
Db 361 CAAGTGCAGGATTTGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420
Qy 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 480
Db 421 AGTGGGGCTGGCGGAGTTTCACAGCTCTATACGGGAGCGGGCCCTGGAGAGGCGCGG 480
Qy 481 CGTCTCGGGAGGGAACTGGSCATCAGTGAGGACAGTCTGACGGGGCCGCTGGCACTG 540
Db 481 CGTCTCGGGAGGGAACTGGSCATCAGTGAGGACAGTCTGACGGGGCCGCTGGCACTG 540
Qy 541 GGGGCCCTGGTAACCTGAGGGCCCTTTTGTGCTAGCAAGTGA 582
Db 541 GGGGCCCTGGTAACCTGAGGGCCCTTTTGTGCTAGCAAGTGA 582
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RESULT 3

```
US-09-809-391-130
; Sequence 130, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 130
; LENGTH: 1864
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1648)
; OTHER INFORMATION: n equals a,t,g, or c
US-09-809-391-130
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```
Query Match 73.5%; Score 428.4; DB 11; Length 1864;
Best Local Similarity 99.3%; Pred. No. 5.5e-108;
Matches 429; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 60
Db 11 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 70
Qy 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120
Db 71 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 130
Qy 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCCACC 180
Db 131 CCGCTGCACCAAGCCATGCGGGCAGCKGGAGATGAGTTCGAGACCCGCTTCGGGGCCACC 190
Qy 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAGCAACGCTTCACC 240
Db 191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAGCAACGCTTCACC 250
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QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db 105 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 164
QY 61 AAGCTGAGCAGAAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCGCAGAGCTGAC 120
Db 165 AAGCTGAGCAGAAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCGCAGAGCTGAC 224
QY 121 CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 160
Db 225 CCGCTGACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 284
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGCTCAGCCCCAGCAACGCTTCACC 240
Db 285 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGCTCAGCCCCAGCAACGCTTCACC 344
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGSCCGCCTTGTAGCCTTCTT 300
Db 345 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGSCCGCCTTGTAGCCTTCTT 404
QY 301 GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
Db 405 GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 464
QY 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGCTGGCTGACTGGATCCACAGC 420
Db 465 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGCTGGCTGACTGGATCCACAGC 524
QY 421 AGTGGGGCTGGG 433
Db 525 AGTGGGGCTGGG 537

RESULT 6
US-10-029-386-24249
; Sequence 24249, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24249
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72
; OTHER INFORMATION: NT HIT: gil4751151, EVALUE 0.00e+00
US-10-029-386-24249
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Query Match 73.3%; Score 427.2; DB 12; Length 433;
Best Local Similarity 99.3%; Pred. No. 1e-107;
Matches 429; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db 2 ATGGGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 61
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QY 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGSCCCCCGGGAGGGCCCGCAGAGCTGAC 120
Db 62 AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGSCCCCCGGGAGGGCCCGCAGAGCTGAC 121
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 180
Db 222 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 181
QY 182 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGGCTCAGCCCCAACAACGCTTCACC 240
Db 182 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCGAGGCTCAGCCCCAACAACGCTTCACC 241
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGGCCCCAACTGGGSCCGCCTTGTAGCCTTCTTT 300
Db 242 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGSCCGCCTTGTAGCCTTCTTT 301
QY 301 GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360
Db 302 GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 361
QY 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGCTGGCTGACTGGATCCACAGC 420
Db 362 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGCTGGCTGACTGGATCCACAGC 421
QY 421 AGTGGGGCTGG 432
Db 422 AGTGGGGCTGG 433
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RESULT 7
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201
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Query Match 44.1%; Score 257; DB 12; Length 6049;
Best Local Similarity 74.6%; Pred. No. 6.4e-61;
Matches 323; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60
Db 5001 ATGGCGATTTTAGTTTCGGGTTTAGATATACGGGTTTGGTGGTAGATTTTGTAGGTTAT 5060
QY 61 AAGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCCGCAGAGCTGAC 120
Db 5061 AAGTTCAGGTAGAAGGTTATGTTTGTGGAGTTGGTTTCGGGGAGGGTTTAGTAGTTGAT 5120
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACC 180
Db 5121 TCGTTGTATTAAAGTTATGCGGGTAGTTGGAGATGAGTTCGAGATTCGTTTTCGGCGTATT 5180
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; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 27084  
; LENGTH: 151  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2  
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 5.00e-70  
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11  
; OTHER INFORMATION: NT HIT: gi14574571, EVALUE 9.00e-80  
US-10-029-386-27084

Query Match 25.9%; Score 151; DB 12; Length 151;  
Best Local Similarity 100.0%; Pred. No. 5.8e-32;  
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 432 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCGCGTCTGCGGGA 491  
|||||  
Db 1 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCGCGTCTGCGGGA 60  
  
QY 492 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGT 551  
|||||  
Db 61 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGT 120  
  
QY 552 AACTGTAGGGCCCTTTTGTGCTAGCAAGTGA 582  
|||||  
Db 121 AACTGTAGGGCCCTTTTGTGCTAGCAAGTGA 151

RESULT 11  
US-09-864-761-17690  
; Sequence 17690, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aomica-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 17690  
; LENGTH: 150  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL049829.2  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1  
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.5  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1  
; OTHER INFORMATION: NT HIT: D87461.1, EVALUE 2.00e-79  
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 8.00e-70  
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11  
US-09-864-761-17690

Query Match 25.7%; Score 150; DB 9; Length 150;  
Best Local Similarity 100.0%; Pred. No. 1.1e-31;  
Matches 150; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 433 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCGCGTCTGCGGGA 492  
|||||  
Db 1 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCGCGTCTGCGGGA 60  
  
QY 493 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGTA 552  
|||||  
Db 61 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGTA 120  
  
QY 553 ACTGTAGGGCCCTTTTGTGCTAGCAAGTGA 582  
|||||  
Db 121 ACTGTAGGGCCCTTTTGTGCTAGCAAGTGA 150

RESULT 12  
US-10-169-223-13  
; Sequence 13, Application US/10169223  
; Publication No. US20030152946A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIMIZU, Shigeomi  
; APPLICANT: TSUJIMOTO, Yoshihide  
; TITLE OF INVENTION: BH4-Fused Polypeptides  
; FILE REFERENCE: 1422-0537P  
; CURRENT APPLICATION NUMBER: US/10/169,223  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: JP 11-371449  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09274  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 13  
; LENGTH: 636  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthesized DNA for mutant bcl-xl  
; NAME/KEY: CDS



```

; LOCATION: (1)..(636)
; OTHER INFORMATION:
US-10-169-223-13
Query Match      22.5%; Score 131; DB 12; Length 636;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGT 157
Db 167 CCCGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGCGGACGAGT 226
QY 158 TCGAGACCCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAG 217
Db 227 TTGAAGTGGGTACCGCGGGCATTCAGTGACCTGACATCCAGCTCCACATCACCCAG 286
QY 218 GCTCAGCCCCAGCAACGCTTCACCCAGGTCTCCGACGAACCTTTTCAAGGGGCCCCAACT 277
Db 287 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACCTTCCGGGATGGGTAAACT 346
QY 278 GGGCGCGCCTTGTAGCCCTCTTTGTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACA 337
Db 347 GGGGTGCGATTGTGGCCCTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGCCTAGACA 406
QY 338 AGGAGATGGAACCACTGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACTGGAGACGC 397
Db 407 AGGAGATGCAGGTATTGGTGAGTCCGATCGCATCGCAGCTTGGATGGCCACTTACTGAATGACC 466
QY 398 GGCTGGCTGACTGGATCCACAGCAGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGG 457
Db 467 ACCTAGAGCCTTGGATCCAGGAGAACGGCGCTGGGATACTTTTGTGMACTCTATGGGA 526
QY 458 ACGGGGCCCTGGAGAGCGCGCGTCTCTCGGAGGGGAACCTGGGCATCAGTGAGGACAG 517
Db 527 ACAATGCAGCAGCCGAGAGCCGAAAGGGCCAGGACGCTTCAACCGCTGGTTCCTGACGG 586
QY 518 TGCTGACGGGGCCG 532
Db 587 GCATGACTGTGGCCG 601

RESULT 13
US-09-959-987-9
; Sequence 9, Application US/09959987
; Publication No. US20030040012A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: A Detection Method of Protein-Protein Interaction
; FILE REFERENCE: 2001_1695A/WMC/00653
; CURRENT APPLICATION NUMBER: US/09/959,987
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/JPO1/01973
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(702)
US-09-959-987-9
Query Match      22.5%; Score 131; DB 11; Length 702;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGT 157
Db 230 CCCGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGCGGACGAGT 289
QY 158 TCGAGACCCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAG 217
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Db 290 TTGAAGTGGGTACCGGGCGGCATTTCAGTGACCTGACATCCCAGTCCACATCACCCAG 349
QY 218 GCTCAGCCCCAGCAACGCTTCACCCAGGTCTCCGACGAACCTTTTCAAGGGGCCCCAACT 277
Db 350 GGACAGCATATCAGAGCTTTGAACAGGTAGTGAATGAACCTTCCGGGATGGGTAAACT 409
QY 278 GGGCGCGCCTTGTAGCCCTTCTTTGTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACA 337
Db 410 GGGGTGCGATTGTGGCCCTTTTCTCCTTCGGCGGGCACTGTGCGTGGAAAGCGTAGACA 469
QY 338 AGGAGATGGAACCACTGTGGGACAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGC 397
Db 470 AGGAGATGCAGGTATTGGTGAGTCGGATCGCAGCTTGGATGGCCACTTACCTGAATGACC 529
QY 398 GGCTGGCTGACTGGATCCACAGCAGTGGGGCTGGCGGAGTTTACAGCTCTATACGGGG 457
Db 530 ACCTAGAGCCTTGGATCCAGGAGAACGGCGCTGGGATACTTTTGTGGAACCTCTATGGGA 589
QY 458 ACGGGGCCCTGGAGAGCGCGCGTCTGCGGAGGGGAACCTGGGCATCAGTGAGGACAG 517
Db 590 ACAATGCAGCAGCCGAGAGCGGAAGGGCCAGGAACGCTTCAACCGCTGGTTCCTGACGG 649
QY 518 TGCTGACGGGGCCG 532
Db 650 GCATGACTGTGGCCG 664

RESULT 14
US-09-734-846-1
; Sequence 1, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-734-846-1
Query Match      22.5%; Score 131; DB 9; Length 926;
Best Local Similarity 56.3%; Pred. No. 2e-26;
Matches 245; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 98 CCGGGAGGGCCAGCAGCTGACCCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGT 157
Db 364 CCCGGAGGTGATCCCCATGGCAGCAGTAAAGCAAGCGCTGAGGGAGCGGACGAGT 423
QY 158 TCGAGACCCCGCTTCCGGCGCACCTTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAG 217
Db 424 TTGAAGTGGGTACCGGGCGGCATTTCAGTGACCTGACATCCCAGTCCACATCACCCAG 483
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OM nucleic - nucleic search, using sw model

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Perfect score: 583  
Sequence: 1 atggcgacccagcctcggc.....ctttttgctagcaagtgaa 583

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
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5:	em_estov:*	5:	em_estov:*
6:	em_estpl:*	6:	em_estpl:*
7:	em_estro:*	7:	em_estro:*
8:	em_htc:*	8:	em_htc:*
9:	gb_est1:*	9:	gb_est1:*
10:	gb_est2:*	10:	gb_est2:*
11:	gb_htc:*	11:	gb_htc:*
12:	gb_est3:*	12:	gb_est3:*
13:	gb_est4:*	13:	gb_est4:*
14:	gb_est5:*	14:	gb_est5:*
15:	em_estfun:*	15:	em_estfun:*
16:	em_estom:*	16:	em_estom:*
17:	em_gss_hum:*	17:	em_gss_hum:*
18:	em_gss_inv:*	18:	em_gss_inv:*
19:	em_gss_pln:*	19:	em_gss_pln:*
20:	em_gss_vrt:*	20:	em_gss_vrt:*
21:	em_gss_fun:*	21:	em_gss_fun:*
22:	em_gss_mam:*	22:	em_gss_mam:*
23:	em_gss_mus:*	23:	em_gss_mus:*
24:	em_gss_pro:*	24:	em_gss_pro:*
25:	em_gss_rod:*	25:	em_gss_rod:*
26:	em_gss_phg:*	26:	em_gss_phg:*
27:	em_gss_vrl:*	27:	em_gss_vrl:*
28:	gb_gss1:*	28:	gb_gss1:*
29:	gb_gss2:*	29:	gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554.8	95.2	804	9 AL157542	AL157542 DKFZp761D
2	553.2	94.9	1030	10 BE793530	BE793530 601590016
3	527.6	90.5	1949	11 AK015644	AK015644 Mus muscu
4	527.6	90.5	3487	11 AK004680	AK004680 Mus muscu

5	525	90.2	969	14	BY715200	BY715200
6	488.2	83.7	697	12	BI770566	BI770566 EC3060362
7	470.4	80.7	967	13	BU503850	BU503850 AGENCOURT
8	447.8	76.8	626	14	CA391923	CA391923 cs20c09.y
9	422.4	72.5	643	12	BI910270	BI910270 EC3069493
10	400.2	68.6	815	10	BF785386	BF785386 602111725
11	386.6	66.3	623	14	CB578463	CB578463 AMGNNUC:N
12	380.2	65.2	854	11	AK013244	AK013244 Mus muscu
13	369	63.3	792	10	BG298789	BG298789 602396527
14	364.8	62.6	548	14	CA407899	CA407899 1004048 H
15	363.8	62.4	869	13	BU557268	BU557268 AGENCOURT
16	363.8	62.4	872	13	BU557410	BU557410 AGENCOURT
17	362	62.1	540	9	AW258810	AW258810 um74a02.y
18	336.8	57.8	437	14	CB790932	CB790932 AMGNNUC:N
19	336	57.6	440	14	CB749817	CB749817 AMGNNUC:N
20	328.4	56.3	758	12	BI764428	BI764428 603050701
21	322.6	55.3	1053	13	BU931540	BU931540 AGENCOURT
22	306.8	52.6	559	14	BY704881	BY704881
23	295.4	50.7	645	14	BY740551	BY740551 BY740551
24	294.8	50.6	601	10	BF204905	BF204905 601866718
25	294.2	50.5	749	10	BG677345	BG677345 602624059
26	294	50.4	410	14	CB804140	CB804140 AMGNNUC:N
27	289.6	49.7	362	9	AA596919	AA596919 vo21f08.f
28	284.2	48.7	1064	13	BQ646339	BQ646339 AGENCOURT
29	269.6	46.2	460	13	BY285647	BY285647 BY285647
30	266	45.6	449	13	BY253191	BY253191 BY253191
31	257.6	44.2	433	9	AW326901	AW326901 20104 MAR
32	257.4	44.2	430	14	CB760687	CB760687 AMGNNUC:N
33	241.6	41.4	457	10	BB856021	BB856021 BB856021
34	241.4	41.4	853	14	CA984774	CA984774 AGENCOURT
35	240.6	41.3	353	13	BY312773	BY312773 BY312773
36	233.2	40.0	425	13	BY251598	BY251598 BY251598
37	232.2	39.8	467	13	BY253189	BY253189 BY253189
38	229.6	39.4	302	13	BY356166	BY356166 BY356166
39	229.2	39.3	452	14	CB786193	CB786193 AMGNNUC:N
40	227	38.9	305	13	BY356183	BY356183 BY356183
41	217.6	37.3	375	13	BY302913	BY302913 BY302913
42	215.6	37.0	372	13	BY133304	BY133304 BY133304
43	211.2	36.2	314	13	BY356000	BY356000 BY356000
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45	201.4	34.5	601	12	BM191403	BM191403 daJ86a10.

ALIGNMENTS

RESULT 1  
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LOCUS DKFZp761D0816\_r1 761 (synonym: hamy2) Homo sapiens cDNA clone  
DEFINITION DKFZp761D0816 5', mRNA sequence.  
ACCESSION AL157542  
VERSION AL157542.1 GI:7057943  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 804)  
AUTHORS Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.  
TITLE EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)  
JOURNAL Unpublished  
COMMENT Contact: Ansorge W  
MIPS

Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by EMBL (European Molecular Biology Laboratories,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No si sequence available.  
This clone (DKFZp761D0816) is available at the R2PD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source  
1. .804  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone\_lib="761 (synonym: hamy2)"  
/note="Vector: pSport1; Site\_1: NotI; Site\_2: SalI"  
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ORIGIN

Query Match 95.2%; Score 554.8; DB 9; Length 804;  
Best Local Similarity 99.1%; Pred. No. 6.9e-120;  
Matches 578; Conservative 0; Mismatches 3; Indels 2; Gaps 2;  
QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Db |||||  
134 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 193  
QY 61 AAGCTGAGGCAGAGGTTATGTCTGTGGAGTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
Db |||||  
194 AAGCTGAGGCAGAGGTTATGTCTGTGGAGTGGCCCCGGGAGGGCCAGCAGCTGAC 253  
QY 121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 180  
Db |||||  
254 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 313  
QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCGAAGCGTTAC 240  
Db |||||  
314 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCGAAGCGTTAC 373  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 300  
Db |||||  
374 CAGGTCTCCGATGAACCTTTTCAAGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 433  
QY 301 GTCTTTGGGCTGCATGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360  
Db |||||  
434 GTCTTTGGGCTGCATGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 493  
QY 361 CAAGTGCAGGAGTGGATGTGTGGCTACCTGGAGACGGCTGGCTGACTGGATCCACAGC 420  
Db |||||  
494 CAAGTGCAGGAGTGGATGTGTGGCTACCTGGAGACGGCTGGCTGACTGGATCCACAGC 553  
QY 421 ACTGGGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGCCCTGGAGAGGCGCGG 480  
Db |||||  
554 ACTGGGGCTGGCGGAGTTCACAGCTCTATACGGGAC - GGGCCCTGGAGAGGCGCGG 612  
QY 481 CGTCTCGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCGCTGGCACTG 540  
Db |||||  
613 CGTCTCGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCGCTGGCACT - 671  
QY 541 GGGGCCCTGGTAACCTGAGGGCCCTTTTGTGCTAGCAAGTGAA 583  
Db |||||  
672 GGGGCCCTGGTAACCTGAGGGCCCTTTTGTGCTAGCAAGTGAA 714

RESULT 2  
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LOCUS BE793530 1030 bp mRNA linear EST 20-SEP-2000  
DEFINITION 601590016F1 NIH\_YGC\_7 Homo sapiens cDNA clone IMAGE:3944307 5',  
mRNA sequence.  
ACCESSION BE793530  
VERSION BE793530.1 GI:10214832  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1030)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
Plate: LLCM800 row: p column: 04  
High quality sequence start: 5  
High quality sequence stop: 709.

FEATURES  
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/clone="IMAGE:3944307"  
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/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_7"  
/note="Organ: lung; Vector: pOTB7; Site\_1: XhoI; Site\_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."  
BASE COUNT 190 a 284 c 386 g 170 t  
ORIGIN

Query Match 94.9%; Score 553.2; DB 10; Length 1030;  
Best Local Similarity 96.9%; Pred. No. 1.8e-119;  
Matches 564; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Db |||||  
144 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 203  
QY 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 120  
Db |||||  
204 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 263  
QY 121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 180  
Db |||||  
264 CCACTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 323  
QY 181 TTCTCTGATCTGGCGGCTCAGTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db |||||  
324 TTCTCTGATCTGGCGGCTCAGTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 383  
QY 241 CAGGTCTCCGACGAACCTTTTCAAGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 300  
Db |||||  
384 CAGGTCTCCGATGAACCTTTTCAAGGGGCCCCCACTGGGGCCGCTTGTAGCCTTCTTT 443  
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444 GTCTTTGGGGCTGCACCTGTGTGTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 503  
QY 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420  
Db |||||  
504 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 563  
QY 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCTGGAGGAGGCGCGG 480  
Db |||||  
564 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACGGGCCCTGGAGGAGGCGCGG 623  
QY 481 CGTCTCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCGCTGGCACTG 540



||||| 624 CGTCTGCGGGGGGACTGGGCATCATGTCAGGACAGTCTGACGGGGGGCTGGCACTG 583

||||| 541 GGGGCCCTGGTAACCTAGAGGGCCCTTTTGTGCTAGCAAGTGA 582

||||| 684 GGGGGCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGA 725

AK015644 1949 bp mRNA linear HTC 05-DEC-2002

Mus musculus adult male testis cDNA, RIKEN full-length enriched library, clone:4930488D08 product:Bcl2-like 2, full insert sequence.

AK015644

AK015644.1 GI:12854052

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P. and Hayashizaki, Y.

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, S., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system-384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamataka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, M., Gaasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L. M., Staudli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuno, Y., Aono, H., Baldarelli, R., Barst, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M. F., Brownstein, M. J., Bult, C., Fietcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, C., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Toyo-oka, K., Wang, K. H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S. and Hayashizaki, Y.

Functional annotation of a full-length mouse cDNA collection

Nature 409 (6821), 685-690 (2001)

21085660

11217851

5

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL

Nature 420, 563-573 (2002)

REFERENCE

6 (bases 1 to 1949)

AUTHORS

Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, J., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.

Direct Submission

Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCGAGTTAATTAAATTAATCCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda F1C I. Cloning sites, 5' end: SalI; 3' end: BamHI. Host: DH10B.

Location/Qualifiers

1. 1949

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/db\_xref="MGI:1897773"

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/clone="4930488D08"

/sex="male"

/tissue type="testis"

/clone\_lib="RIKEN full-length enriched mouse cDNA library"

/dev\_stage="adult"

132..713

/note="unnamed protein product; Bcl2-like 2

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BASE COUNT 396 a 473 c 628 g 452 t

ORIGIN

Query Match 90.5%; Score 527.6; DB 11; Length 1949;

Best Local Similarity 94.2%; Pred. No. 2.1e-113;

Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 1 ATGGGACCCCGACCTCGGCCCGAGACACACGGGCTCTGGTGGCAGACTTGTAGGTTAT 60  
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Db 132 ATGGGACCCCGACCTCAACCCCGAGACACACGGGCTCTAGTGGTGACTTGTAGGCTAT 191  
Qy 61 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCCGGGGAGGGCCCGCAGCAGCTGAC 120  
|||||  
Db 192 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCACGCCGCCGAC 251  
Qy 121 CCGCTGCACCAAGCCATGCGGCAGCTGGAGATGATTCGAGACCCGCTTCGGCGCAC 180  
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Qy 181 TTCTCTGATCTGGCGGCTCAGCTGCAITGTGACCCCGAGCTCAGCCCGCAGCAACGCTTCACC 240  
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Db 312 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGCTCAGCCCGCAGCAACGCTTCACC 371  
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Db 372 CAGGTTCGACGAACCTTTTCAAGGGGGCCCCCAACTGGGGCGCGTCTTGTGSCATCTTT 431  
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Db 432 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTGGTGGGA 491  
Qy 361 CAAGTGACGAGTGGATGGTGGCTACCTGGAGACGGCGCTGGCTGACTGGATCCACAGC 420  
|||||  
Db 492 CAAGTGACGAGTGGATGGTGGCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 551  
Qy 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCGG 480  
|||||  
Db 552 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGCGCACGG 611  
Qy 481 CGTCTCGGAGGGGAACCTGGCATCAGTGAGGACAGTGTCTGCTACGGGGCGCTGGCACTG 540  
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Db 612 CGTCTCGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTCTGCTACGGGGCGCTGGCACTG 671  
Qy 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582  
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Db 672 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 713

RESULT 4  
AK004680  
LOCUS  
DEFINITION  
AK004680 3487 bp mRNA linear HTC 05-DEC-2002  
Mus musculus adult male lung cDNA, RIKEN full-length enriched  
library, clone:120009L24 product:Bcl2-like 2, full insert  
sequence.  
AK004680  
VERSION  
AK004680.1 GI:12836027  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
1  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
2  
99279253  
PUBMED  
10349636  
REFERENCE  
2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
3  
20499374  
PUBMED  
11042159  
REFERENCE  
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Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
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Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
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Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
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11076861  
REFERENCE  
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Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,  
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Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,  
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,  
Hofmann,M., Hume,D.A., Kamiya,X., Lee,N.H., Lyons,P.,  
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Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,  
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Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S.  
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Nature 409 (6821), 685-690 (2001)  
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PUBMED  
11217851  
REFERENCE  
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The PANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation:  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 3487)  
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,  
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itch,M., Izawa,Y.,  
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,  
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
Please visit our web site (http://genome.gsc.riken.go.jp/) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5' GAGAGAGAGCGCGCGCAACTCGAGTTTTTTTTTTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. Second  
strand cDNA was prepared with the primer adapter of sequence[5'  
GAGAGAGAGGATCCAGAGCTCAATTAATTTAATAACCCCCCCC 3']. cDNA was  
cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end:

FEATURES

source

XhoI. Host: SCLR.

Location/Qualifiers

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Best local Similarity 94.2%; Pred. No. 2.5e-113;

Matches 548; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

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QY 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGGCTCAGCCAGCAACGCTCACC 240

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Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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QY 301 GTCTTTGGGGCTGCACTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 360

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509 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTTGGTGGGA 568

QY 361 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGGGCTGGCTGACTGGATCCACAGC 420

Db ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||

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689 CGTCTGCGGAGGGGAACCTGGGCGATCAGTGAGGACAGTGTGACGGGGCGGTGGCACTG 748

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749 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAACTGA 790

RESULT 5

BY715200

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 969)

REFERENCE

AUTHORS

Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I., Kiyosawa,H., Yagi,K., Tomaru,Y., Hasegawa,Y., Nogami,A., Schonbach,C., Gojobori,T., Baldarelli,R., Hill,D.P., Bult,C., Hume,D.A., Quackenbush,J., Schriml,L.M., Kanapin,A., Matsuda,H., Batalov,S., Beisel,K.W., Blake,J.A., Bradt,D., Brusic,V., Chothia,C., Corbani,L.E., Cousins,S., Dalia,E., Dragani,T.A., Fletcher,C.F., Forrest,A., Frazer,K.S., Gaasterland,T., Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S., Gustincich,S., Hirokawa,N., Jackson,I.J., Jarvis,E.D., Kanai,A., Kawaji,H., Kawasawa,Y., Kedzierski,R.M., King,B.L., Konagaya,A., Kurochkin,I.V., Lee,Y., Lenhard,B., Lyons,P.A., Maglott,D.R., Maltais,L., Marchionni,L., McKenzie,L., Miki,H., Nagashima,T., Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G., Petrovsky,N., Pillai,R., Pontius,J.U., Qi,D., Ramachandran,S., Ravasi,T., Reed,J.C., Reed,D.J., Reid,J., Ring,B.Z., Ringwald,M., Sandelin,A., Schneider,C., Sempile,C.A., Setou,M., Shimada,K., Sultana,R., Takenaka,Y., Taylor,M.S., Teasdale,R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolan,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

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12466851

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Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp,

URL:http://genome.gsc.riken.go.jp/

Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA  
encyclopedia: real-time sequence clustering for construction of a  
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site (<http://genome.gsc.riken.go.jp>) for  
further details.

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Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in  
RIKEN. Division of Experimental Animal Research in Riken  
contributed to prepare mouse tissues. 1st strand cDNA was  
primed with a primer [5'  
GAGAGAGAGAGGATCCAGAGCTCTTTTCTTTTCTTTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse  
transcriptase and subsequently enriched for full-length by  
cap-trapper. Second strand cDNA was prepared with the  
primer adapter of sequence [5'  
GAGAGAGAGAGCGCGCAATTATTCGAGTTAATTAAATTATCCCCCCCC  
3']. cDNA was cloned into the XhoI and BamHI sites. "  
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ORIGIN  
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Matches 547; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
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VERSION BI770566.1 GI:15762144  
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ORGANISM Homo sapiens  
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1 (bases 1 to 697)  
NIH-MGC <http://mgc.ncbi.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC);  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-romail.nih.gov](mailto:cgapbs-romail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM11526 row: k column: 15  
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upon cloning). Average insert size 1.4 kb, insert size  
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RESULT 7  
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LOCUS  
DEFINITION  
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BU503850  
VERSION  
BU503850.1 GI:22810083  
EST.  
SOURCE  
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ORGANISM  
Mus musculus  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 967)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LL4V14043 row: c column: 23  
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Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.

BASE COUNT 199 a 255 c 348 g 165 t  
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Matches 547; Conservative 0; Mismatches 36; Indels 5; Gaps 5;  
  
QY 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTAT 60  
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QY 61 AAGCTGAGGAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 120  
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Db 190 AAGCTGAGGAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCGCCGAC 249  
  
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LOCUS  
DEFINITION  
CA391923 626 bp mRNA linear EST 06-NOV-2002  
cs20c09.y1 Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified); cs Homo sapiens cDNA clone cs20c09  
5', mRNA sequence.  
CA391923  
VERSION  
CA391923.1 GI:24724221  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 626)  
REFERENCE  
AUTHORS  
Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Behal,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
Expressed sequence tag analysis of human RPE/choroid for the  
NEIBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
MEDLINE  
22103460  
PUBMED  
12107410  
COMMENT  
Contact: Wistow G  
Section on Molecular Structure and Function

National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 20 row: c column: 09  
Seq primer: M13RPl reverse primer (ABI).  
Location/Qualifiers

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source

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eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>. The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."  
108 a 202 c 197 g 118 t 1 others

BASE COUNT 108 a 202 c 197 g 118 t 1 others  
ORIGIN  
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Best Local Similarity 99.3%; Pred. No. 8.2e-95;  
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175 ATGGCGACCCAGCCCTCGGCCCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGTTAT 234  
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235 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 294  
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295 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGATCGAGACCCGCTTCGGCGGCACC 354  
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355 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGCAGCTTCACC 414  
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415 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCCCTTGTAGCCTTCTTT 474  
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535 CAAGTGCAGGAGTGGATGGTGGCCTACCTGGAGACGGGGCTGGCTGACTGGATCCACAGC 594  
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Db |||||||  
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RESULT 9  
BI910270

LOCUS BI910270 643 bp mRNA linear EST 16-OCT-2001  
DEFINITION 603069493F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5218294 5',  
mRNA sequence.  
ACCESSION BI910270  
VERSION BI910270.1 GI:16173653  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 643)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM11548 row: j column: 23  
High quality sequence stop: 643.

FEATURES  
source

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(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH MGC Library."  
129 a 184 c 216 g 114 t

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Matches 449; Conservative 0; Mismatches 26; Indels 1; Gaps 1;

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200 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 259  
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260 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGATCGAGACCCGCTTCGGCGGCACC 319  
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320 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGCAGCTTCACC 379  
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Db |||||||  
380 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCCCTTGTAGCCTTCTTT 439  
QY 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAG-ATGGAACCACTGGTGGG 359  
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QY	420	CAGTGGGGCTGGGGAGTTCAACAGCTCTATACGGGGACGGGCCCTCGAGGAGG	475
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	602111728F1 NCI_CGAP_Kid14 Mus musculus cDNA clone IMAGE:4239798		
	Mus musculus (house mouse)		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
	i (bases 1 to 815)		
	NIH-MGC http://mgc.nci.nih.gov/		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-r@mail.nih.gov		
	Tissue Procurement: Jeffrey E. Green, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
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	166 a 212 C 296 G 141 T		
 BASE COUNT			
ORIGIN			
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QY	81	TGCTCTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGACCCGCTGCACCAGCATCGG	140
D8	61	TGCTCTGGAGCTGGCCCCGGGGAGGGCCCCAGCAGCTGACCCGCTGCACCAGCATCGG	120
QY	141	GGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGGCACCTTCTCTGATCTGGCGGCTCA	200
D8	121	GGCTGCTGGAGACGAGTT-GAGACCCGCTTCGGGGCACCTTCTCTGACCTGGCGGCTCA	179
QY	201	GCTGCATGTGACCCAGGCTCAGCCCGAACCGCTTCACCCAGGCTCCCGACGAACTTTT	260
D8	180	GCTACAGTGAACCCAGGCTCAGCCCGAACCGCTTCACCCAGGCTTCGACGAACTTTT	239

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RESULT 12  
AK013244  
LOCUS  
DEFINITION AK013244 854 bp mRNA linear HTC C5-DEC-2002  
Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length  
enriched library, clone:2810435A13 product:Bcl2-like 2, full insert  
sequence.  
ACCESSION AK013244  
VERSION AK013244.1 GI:12850487  
KEYWORDS HTC; CAP trapper.  
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ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1  
REFERENCE  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,  
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,  
Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,  
Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,  
Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,J., Fukuda,S.,  
Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamanaka,I.,  
Saito,T., Okazaki,Y., Gojobori,T., Bono,H., Kasukawa,T., Saito,R.,  
Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T.,  
Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H.,  
Kuehl,P., Lewis,S., Matsuo,Y., Nikaido,I., Pesole,G.,

Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Tomita,M.,  
Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H.,  
Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N.,  
Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C.,  
Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D.,  
Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P.,  
Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P.,  
Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H.,  
Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H.,  
Toyo-oka,K., Wang,K.H., Weitz,C., Whittaker,C., Wilming,L.,  
Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Khtsuki,S.  
and Hayashizaki,Y.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409 (6921), 685-690 (2001)  
21085660  
11217851  
5  
The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 854)  
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,  
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,  
Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K.,  
Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M.,  
Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,  
Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,  
Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,  
Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D.,  
Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,  
Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,  
Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
Please visit our web site (http://genome.gsc.riken.go.jp/) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
[5' GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTNN 3'], cDNA was  
prepared by using trehalose thermo-activated reverse transcriptase  
and subsequently enriched for full-length by cap-trapper. cDNA went  
through one round of normalization to Rot = 7.5 and subtraction to  
Rot = 37.5. Second strand cDNA was prepared with the primer adapter  
of sequence [5'  
GAGAGAGAGATCTCGAGTTAATTAATTAATCCCCCCCCCC 3']. cDNA was cleaved  
with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.  
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CDS



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Db 376 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGCAGCAACGCTTCACC 435  
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Db 496 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 555  
QY 361 CAAGTGAGGAGTGGATGGTGGCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 420  
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DEFINITION 602396527F1 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:4511215 5',  
mRNA sequence.  
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VERSION BG298789.1 GI:13063794  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 792)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapsb@mail.nih.gov](mailto:cgapsb@mail.nih.gov)  
Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM10394 row: e column: 08  
High quality sequence stop: 713.  
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Location/Qualifiers  
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Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC Library."  
BASE COUNT 174 a 201 c 246 g 171 t  
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Db 458 CAAGTGACGAGTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 517  
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DEFINITION 1004048 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens  
cDNA 5', mRNA sequence.  
ACCESSION CA407899  
VERSION CA407899.1 GI:24772770  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 548)  
AUTHORS Yang,R.-Z., Shuldiner,A. and Gong,D.-W.  
TITLE EST analysis of human adipose gene expression

JOURNAL COMMENT

Unpublished  
Contact: Gong Da-Wei  
Division of Endocrinology, Diabetes and Nutrition  
University of Maryland  
660 Redwood St., H497, Baltimore, MD 21201, USA  
Tel: 410 706 1672  
Fax: 410 706 1622  
Email: dgong@medicine.umaryland.edu  
PCR Primers  
FORWARD: CTCGGGAAGCGGCCATTGTTGGT  
BACKWARD: AATACGACTCACTATAGGCGAATTGG  
Seq primer: GTTGGTACCGGAATTC.

FEATURES source

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Db 361 TGGCACTGGGGGCCCTGGTA 380

RESULT 15 BU557268

LOCUS BU557268 869 bp mRNA linear EST 16-SEP-2002  
DEFINITION AGENCOURT\_10253293 NIH\_MGC\_109 Homo sapiens cDNA clone  
IMAGE:6585108 5', mRNA sequence.

ACCESSION BU557268

VERSION BU557268.1 GI:22907564

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 869)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LCM2796 row: i column: 12  
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Location/Qualifiers

FEATURES source

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XhoI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGGAG(G). Library constructed by Ling Hong in the  
laboratory of Gerald M. Rubin (University of California,  
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and  
Superscript II RT (Life Technologies). Note: this is a  
NIH\_MGC Library."

BASE COUNT 157 a 219 c 310 g 182 t 1 others  
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Query Match 62.4%; Score 363.8; DB 13; Length 869;  
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Matches 365; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 577 AAGTGAA 583  
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Db 361 AAGTGAA 367

Search completed: October 27, 2003, 13:50:44  
Job time : 1475.26 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:03:45 ; Search time 1735.01 Seconds  
(without alignments)  
13722.924 Million cell updates/sec

Title: US-09-925-674A-8  
Perfect score: 582  
Sequence: 1 atggcgacccagcctcaac.....ccttttttgcctagcaagtga 582

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
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4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:  
15: em\_ba:  
16: em\_fun:  
17: em\_hum:  
18: em\_in:  
19: em\_mu:  
20: em\_om:  
21: em\_or:  
22: em\_ov:  
23: em\_pat:  
24: em\_ph:  
25: em\_pl:  
26: em\_ro:  
27: em\_sts:  
28: em\_un:  
29: em\_vi:  
30: em\_htg\_hum:  
31: em\_htg\_inv:  
32: em\_htg\_other:  
33: em\_htg\_mus:  
34: em\_htg\_pin:  
35: em\_htg\_rod:  
36: em\_htg\_mam:  
37: em\_htg\_vrt:  
38: em\_sy:  
39: em\_htgo\_hum:  
40: em\_htgo\_mus:  
41: em\_htgo\_other:

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
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3	563.4	96.8	581	6	AX022531	AX022531 Sequence
4	563.4	96.8	581	6	AX030819	AX030819 Sequence
5	562.8	96.7	582	10	AF096291	AF096291 Rattus no
6	562.8	96.7	3473	10	AY170344	AY170344 Mus muscu
7	558.2	95.9	579	6	AR020779	AR020779 Sequence
8	524.4	90.1	582	6	AX481423	AX481423 Sequence
9	524.4	90.1	582	9	HSU59747	U59747 Human Bcl-w
10	521.2	89.6	3542	9	D97461	D97461 Human mRNA
11	519.6	89.3	583	6	AX022529	AX022529 Sequence
12	519.6	89.3	583	6	AX030817	AX030817 Sequence
13	519.6	89.3	1437	9	BC021198	BC021198 Homo sapi
14	515	88.5	579	6	AR020780	AR020780 Sequence
15	468.4	80.5	220818	2	AC128940	AC128940 Rattus no
16	468.4	80.5	223933	2	AC097389	AC097389 Rattus no
17	429.8	73.8	3815	10	BC040369	BC040369 Mus muscu
18	429.8	73.8	237561	10	AC116591	AC116591 Mus muscu
19	415.4	71.4	210784	2	AC119293	AC119293 Rattus no
20	415.4	71.4	263901	2	AC115371	AC115371 Rattus no
21	405.6	69.7	148278	2	AC079885	AC079885 Rattus no
22	405.6	69.7	180665	2	AC084240	AC084240 Rattus no
23	405.6	69.7	221557	2	AC134055	AC134055 Rattus no
24	372.8	64.1	1098	6	BD078624	BD078624 Human pro
25	372.2	64.0	196292	9	CNS0000B	AL049829 Human chr
26	241.2	41.4	749	5	XLR1	X82462 X.laavis R1
27	218.6	37.6	6049	6	AX345130	AX345130 Sequence
28	192.6	33.1	6049	6	AX345131	AX345131 Sequence
29	142.4	24.5	1252	4	AB073983	AB073983 Canis fam
30	140.8	24.2	702	4	AY005131	AY005131 Oryctolag
31	140.8	24.2	1163	4	AB080951	AB080951 Felis cat
32	139.2	23.9	766	4	AF164517	AF164517 Ovis arie
33	137.6	23.6	541	4	AF245488	AF245488 Bos tauru
34	136	23.4	541	4	AF245489	AF245487 Bos tauru
35	136	23.4	541	4	AF245489	AF245489 Bos tauru
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37	135	23.2	1742	6	BD012974	BD012974 A mutagen
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42	134.6	23.1	702	6	BD084108	BD084108 Method of
43	134.6	23.1	702	6	BD102202	BD102202 Method fo
44	134.6	23.1	702	9	BT007208	BT007208 Homo sapi
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ALIGNMENTS

RESULT :  
MMU59746  
LOCUS  
DEFINITION Mus musculus Bcl-w (bcl-w) mRNA, complete cds.  
ACCESSION U59746  
VERSION U59746.1 GI:1572494  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE 1 (bases 1 to 582)  
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C., Bernard,O., CopeLand,N.G.,  
Jenkins,N.A., Sutherland,G.R., Baker,E., Adams,J.M. and Cory,S.  
TITLE bcl-w, a novel member of the bcl-2 family, promotes cell survival

JOURNAL Onccgene i3 (4), 665-675 (1996)  
MEDLINE 96358615  
PUBMED 8761287  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Gibson,L., Holmgreen,S.P., Huang,D.C.S., Bernard,O., Adams,J.N. and Cory,S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and Eliza Hall Institute of Medical Research, PO Royal Melbourne Hospital, Parkville, Victoria 3050, Australia  
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QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420  
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QY 421 AGTGGGGCTGGCGGAGTTCACAGCTCTATACGGGGACCGGGCCCTGGAGGACCGG 480  
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QY 481 CGTCTCGGGGAGGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540  
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481 CGTCTCGGGGAGGGGAACCTGGGCATCAGTGAAGACAGTGTGACGGGGCCGTGGCACTG 540

QY 541 GGGGCCCTGGTAACCTAGGGGGCCCTTTTGTAGCAAGTGA 582  
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DEFINITION Mus musculus BCL-W (Bcl-w) mRNA, complete cds.  
ACCESSION AF030769  
VERSION AF030769.1 GI:2623249  
KEYWORDS  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3476)  
AUTHORS Ross,A.J., Waymire,K.G., Moss,J.E., Parlow,A.F., Russell,L.D. and MacGregor,G.R.  
TITLE Bcl-w is required for testis homeostasis  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3476)  
AUTHORS Ross,A.J. and MacGregor,G.R.  
TITLE Direct Submission  
JOURNAL Submitted (21-OCT-1997) Center for Molecular Medicine, Emory University, 1462 Clifton Road, Atlanta, GA 30322, USA  
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/number=4  
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3428..3441  
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Best Local Similarity 99.7%; Pred. No. 2.1e-128;  
Matches 580; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCAACCCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db |||||  
179 ATGGCGACCCAGCCTCAACCCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 238







ACCESSION AY170344  
VERSION AY170344.1 GI:27497698  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 3473)  
AUTHORS Su,H.-Y.  
TITLE Extraction from neonatal mouse skin after IGF-1 stimulation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3473)  
AUTHORS Su,H.-Y.  
TITLE Direct Submission  
JOURNAL Submitted (29-OCT-2002) Biotechnology, Pingtung University, No. 1, Hsueh Fu Road, Nei-Pu Hsiang, Pingtung, Taiwan 912, Taiwan  
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BASE COUNT 758 a 831 c 1021 g 863 t  
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Best Local Similarity 97.9%; Pred. No. 1.5e-124;  
Matches 570; Conservative 0; Mismatches 12; Indels 0; Gaps 0;  
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DEFINITION Sequence 1 from patent US 5789201.  
ACCESSION AR020779  
VERSION AR020779.1 GI:3975394  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 579)  
AUTHORS Guastella,J.  
TITLE Genes coding for bcl-y a bcl-2 homologue  
JOURNAL Patent: US 5789201-A : 04-AUG-1998;  
FEATURES Location/Qualifiers  
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Best Local Similarity 97.8%; Pred. No. 2.4e-123;  
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DEFINITION Sequence 37 from Patent WO02055693.  
ACCESSION AX481423  
VERSION AX481423.1 GI:22316337  
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ORGANISM Homo sapiens  
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REFERENCE 1  
AUTHORS Kreutzer, R., Limmer, S., Rost, S. and Hadwiger, P.  
TITLE Method for inhibiting the expression of a target gene  
JOURNAL Patent: WO 02055693-A 37 18-JUL-2002;  
Ribopharma AG (DE)  
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Best Local Similarity 93.8%; Pred. No. 3e-115;  
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LOCUS HSU59747 582 bp mRNA linear PRI 29-SEP-1996  
DEFINITION Human Bcl-w (bcl-w) mRNA, complete cds.  
ACCESSION U59747  
VERSION U59747.1 GI:1572492  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
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REFERENCE 1 (bases 1 to 582)  
AUTHORS Gibbons, L., Holmgreen, S.P., Huang, D.C., Bernard, O., Copeland, N.G.,  
Jenkins, N.A., Sutherland, G.R., Baker, E., Adams, J.M. and Cory, S.  
TITLE bcl-w, a novel member of the bcl-2 family, promotes cell survival  
JOURNAL Oncogene 13 (4), 665-675 (1996)  
MEDLINE 96358615  
PUBMED 8761287  
REFERENCE 2 (bases 1 to 582)  
AUTHORS Gibbons, L., Holmgreen, S.P., Huang, D.C.S., Bernard, O., Adams, J.M. and  
Cory, S.  
TITLE Direct Submission  
JOURNAL Submitted (03-JUN-1996) Molecular Biology Unit, The Walter and  
Eliza Hall Institute of Medical Research, PO Royal Melbourne  
Hospital, Parkville, Victoria 3050, Australia  
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BASE COUNT 104 a 156 c 211 g 111 t  
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Query Match 90.1%; Score 524.4; DB 9; Length 582;  
Best Local Similarity 93.8%; Pred. No. 3e-115;  
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCAACCCCGACACACACGGGCTCTAGTGGTGACTTTGTAGGCTAT 60  
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DEFINITION  
ACCESSION D87461  
VERSION D87461.1 GI:1944417  
KEYWORDS KIAA0271.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Nagase,T., Seki,N., Ishikawa,K., Ohira,M., Kawarabayashi,Y.,  
Ohara,O., Tanaka,A., Kotani,H., Miyajima,N. and Nomura,N.  
TITLE Prediction of the coding sequences of unidentified human genes. VI.  
The coding sequences of 80 new genes (KIAA0201-KIAA0280) deduced by  
analysis of cDNA clones from cell line KG-1 and brain  
DNA Res. 3 (5), 321-329 (1996)  
JOURNAL  
MEDLINE 97191544  
PUBMED 9039502  
REFERENCE 2 (bases 1 to 3542)  
AUTHORS Ohara,O., Nagase,T., Kikuno,R. and Nomura,N.  
TITLE Direct Submission  
JOURNAL Submitted (27-AUG-1996) Osamu Ohara, Kazusa DNA Research Institute;  
1532-3, Yana, Kisarazu, Chiba 292-0812, Japan  
(E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)  
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Best Local Similarity 93.5%; Pred. No. 1.4e-114;

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RESULT 11  
LOCUS AX022529 583 bp DNA linear PAT 07-SEP-2000  
DEFINITION Sequence 6 from Patent EP0932674.  
ACCESSION AX022529  
VERSION AX022529.1 GI:10046125  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
unclassified.  
REFERENCE 1  
AUTHORS Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.  
TITLE A novel mammalian gene, bcl-w, belongs to the bcl-2 family of  
apoptosis-controlling genes  
JOURNAL Patent: EP 0932674-A 6 04-AUG-1999;  
AYRAD OPERATIONS PTY LTD (AU)  
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RESULT 12
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LOCUS
DEFINITION      Sequence 6 from Patent WO9735971.
ACCESSION      AX030817
VERSION
KEYWORDS
SOURCE      unidentified
ORGANISM      unidentified.
REFERENCE
AUTHORS      Adams,J.M., Holmgreen,S.P., Cory,S. and Gibson,L.M.
TITLE      A novel mammalian gene, bcl-w, belongs to the bcl-2 family of
JOURNAL      apoptos-s-controlling genes
ADAMS JERRY MCKEE (AU) ; HOLMGREEN SHAUN P (AU) ; CORY SUZANNE (AU)
; GIBSON LEONIE M (AU) ; AMRAD OPERATIONS PTY LTD (AU)
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BASE COUNT      105 a      157 c      210 g      111 t
ORIGIN
Query Match      89.3%;      Score 519.6;      DB 6;      Length 583;
Best Local Similarity 93.3%;      Pred. No. 4.3e-114;
Matches 543;      Conservative 0;      Mismatches 39;      Indels 0;      Gaps 0;

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QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGAAAGGCCAGCGCCGAC 120
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QY 121 CCGCTGACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCGCACC 180
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QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420
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QY 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAGTGA 582
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RESULT 13
BC021198      1437 bp      mRNA      linear      PRI 22-JAN-2002
LOCUS
DEFINITION      Homo sapiens, BCL2-like 2, clone MGC:10675 IMAGE:3944307, mRNA,
complete cds.
ACCESSION      BC021198
VERSION      BC021198.1 GI:18203706
KEYWORDS      MGC.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1437)
Strausberg,R.
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
```

REMARK  
COMMENT  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center: (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc.mgc@nhgri.nih.gov](mailto:nisc.mgc@nhgri.nih.gov)  
Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,  
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
Lim, M., Maduro, Q.L., Masiello, C., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Snyder, B., Startripop, S., Thomas, P.J.,  
Tiongson, E.E., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A.,  
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 15 Row: k Column: 19  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 14574571.

FEATURES  
source

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/db\_xref="LocusID:599"  
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/clone\_lib="NIH MGC 7"  
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303 a 343 c 509 g 282 t

CDS

Query Match 89.3%; Score 519.6; DB 9; Length 1437;  
Best Local Similarity 93.3%; Pred. No. 3.8e-114;  
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
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QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db 356 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 415  
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RESULT 14  
AR020780

LOCUS AR020780 579 bp DNA linear PAZ 05-DEC-1998  
DEFINITION Sequence 2 from patent US 5789201.  
ACCESSION AR020780  
VERSION AR020780.1 GI:3975395

KEYWORDS

SOURCE Unknown.

ORGANISM

Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 579)

AUTHORS Guastella, J.

TITLE Genes coding for bcl-y a bcl-2 homologue

JOURNAL Patent: US 5789201-A 2 04-AUG-1998;

FEATURES Location/Qualifiers

source 1..579

/organism="unknown"

BASE COUNT 106 a 154 c 208 g 111 t

ORIGIN

Query Match 88.5%; Score 515; DB 6; Length 579;  
Best Local Similarity 93.1%; Pred. No. 5.4e-113;  
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
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Db 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGAAGACTTTGTAGGTTAT 60  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120  
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QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTTCCTAGCAAG 579

Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTTCCTAGCAAG 579

RESULT 15

AC128940

LOCUS

DEFINITION Rattus norvegicus clone CH230-43402, \*\*\* SEQUENCING IN PROGRESS

\*\*\*, 4 unordered pieces.

AC128940

AC128940.3 GI:25073546

HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.

Rattus norvegicus (Norway rat)

SOURCE Rattus norvegicus

ORGANISM

REFERENCE

AUTHORS

Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Arguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,P., Biswal,K., Blair,J., Burch,P., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,S., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Far,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hires,S., Hladur,S.L., Hodgson,A., Hogues,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,C., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,S., Lorensuhewa,L., Loulseghe,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,X.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.C.,

Weinstock,G. and Gibbs,R.A.

Direct Submission

Unpublished

REFERENCE 2 (bases 1 to 220818)

Worley,K.C.

Direct Submission

Submitted (24-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 220818)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23269386.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: KBEM

Center clone name: CH230-43402

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 202395 bases at least Q40

Consensus quality: 205627 bases at least Q30

Consensus quality: 207823 bases at least Q20

Estimated insert size: 212631; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

\* 1 174472: contig of 174472 bp in length

\* 174473 174572: gap of unknown length

\* 174573 218266: contig of 43694 bp in length

\* 218267 218366: gap of unknown length

\* 218367 219597: contig of 1231 bp in length

\* 219598 219697: gap of unknown length

\* 219698 220818: contig of 1121 bp in length.

Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-43402"

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/note="wgs contig"

misc\_feature

BASE COUNT 62390 a 42027 c 41606 g 62941 t 11854 others

ORIGIN

Query Match 80.5%; Score 468.4; DB 2; Length 220818;



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QY	121	CCGCTGACCAAGCCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTCCCGCCGACC	180
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QY	361	CAAGTGCAGGATTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC	420
Db	142346	CAAGTGCAGGACTGGATGGTGGCTACCTGGAGACATGCTGACTGACTGGATCGACAGC	142405
QY	421	AGTGGGGCTGGCGGAGTTCAAGCTCTATACGGGGACGGGGCCCTGGAGGAGGACCGG	480
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QY	541	GGGGCCCTGGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAGTGA	582
Db	142511	GGAGCCCTGGTAACCTGTAGGGGCCCTTTTGTGCTAGCAAGTGA	142552

GenCore version 5.1.6  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:02:30 ; Search time 176.848 Seconds  
(without alignments)  
8883.744 Million cell updates/sec

Title: US-09-925-674A-8  
Perfect score: 582  
Sequence: i atggcgacccagcctcaac.....cctttttgctagcaagtga 582

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_19Jun03:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	558.2	95.9	579	19	AAV283333
5	558.2	95.9	579	20	AAV283333
6	524.4	90.1	582	24	ABX09972
7	524.4	90.1	582	24	ABV78153
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9	524.4	90.1	582	24	ABL91694	Human polynucleoti
10	521.2	89.6	3542	25	ABT16642	Human bcl-2 gene S
11	520.2	89.4	581	20	AAV251132	Human bcl-w gene.
12	519.6	89.3	583	18	AAV251134	Human bcl-w gene d
13	519.6	89.3	583	20	AAV251134	Human bcl-w gene d
14	515	88.5	579	19	AAV283334	Human bcl-y gene.
15	515	88.5	579	20	AAV283334	Human bcl-y gene.
16	372.8	64.1	1098	19	AAV41925	cDNA encoding the
17	372.4	64.0	1864	19	AAV59630	Nucleotide sequenc
18	372.4	64.0	1864	24	ABS73617	Human secreted pro
19	218.6	37.6	6049	24	ABL32228	Human CDNA #1 for
20	192.6	33.1	6049	24	ABL32229	Human immune syste
21	148.4	25.5	150	22	ABA47382	Human immune syste
22	148.4	25.5	150	22	ABA47382	Human breast cell
23	148.4	25.5	150	22	ABA65269	Human foetal liver
24	148.4	25.5	150	22	AAK13683	Probe #10836 for g
25	148.4	25.5	150	22	AAK39424	Human brain expres
26	148.4	25.5	150	22	AAI20236	Human bone marrow
27	148.4	25.5	150	22	AAI20236	Probe #10169 for g
28	148.4	25.5	150	22	AAI45438	Probe #14124 used
29	148.4	25.5	150	22	AAI05940	Probe #5931 used t
30	148.4	25.5	150	23	ABS39016	Human liver single
31	135	23.2	1742	22	ABS13513	Human genome-deriv
32	134.6	23.1	636	22	AAF75960	Rat wild-type bcl-
33	134.6	23.1	702	22	AAH48169	Mutant bcl-XL codi
34	134.6	23.1	926	16	AAQ81698	cDNA clone HP03564
35	134.6	23.1	926	17	AAT4C079	Human thymus BCL-X
36	134.6	23.1	926	21	AAZ93614	Bcl-XL gene. Homo
37	134.6	23.1	926	22	AAS15189	Bcl-x gene. Homo
38	134.6	23.1	926	22	AAC90810	Human bcl-x cDNA.
39	134.6	23.1	926	24	ABK84766	Human Bcl-XL nucle
40	134.6	23.1	926	25	ABT16641	Human cDNA differe
41	134.6	23.1	1236	22	AAS00247	Human bcl-2 gene S
42	134.6	23.1	7372	20	AAV33182	Bcl-XL-DTR apoptos
43	131.2	22.5	1455	22	AAS00250	Base sequence of t
44	129.6	22.3	747	22	AAF30926	LFr-Bcl-XL apoptos
45	126.8	21.8	600	22	ABA60917	Human Bcl-XL (tran
						Human foetal liver

ALIGNMENTS

RESULT 1:  
AAV251133  
ID AAV251133 standard; DNA; 581 BP.  
XX AAV251133;  
XX AAV251133;  
XX 05-JUL-1999 (first entry)  
DT Mouse bcl-w gene.  
DE Mouse bcl-w gene.  
XX Spermatoogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;  
KW animal model; ss.  
XX MUs sp.  
XX WO9913710-A1.  
XX 25-MAR-1999.  
PD 16-SEP-1998; 98WO-AU00764.  
XX 16-SEP-1997; 97AU-0009228.  
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA Adams J, Cory S, Gibson L, Koentgen P, Print C;  
PI WPI; 1999-243890/20.  
DR P-PSDB; AAY05531.  
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or

PT protein associated with Bcl-w  
XX Claim 3; Page 34; 52pp; English.  
XX

CC The present sequence is the mouse bcl-w gene encoding Bcl-w protein  
CC (see AAY05531), a pro-survival member of the Bcl-2 family which is  
CC widely expressed and which is essential for spermatogenesis. The  
CC invention relates generally to a method of treatment and to an  
CC animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male  
CC animals. Methods are provided for the treatment of infertility, or  
CC for reducing fertility, by modulating spermatogenesis. An animal  
CC model carries a mutation is at least one allele of the human or  
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals  
CC have disorganised seminiferous tubules and are substantially  
CC infertile, but possess no other major abnormalities as determined  
CC by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of  
CC inducing, enhancing or otherwise facilitating spermatogenesis in  
CC animals, or which can induce infertility.

XX Sequence 581 BP; 106 A; 158 C; 200 G; 117 T; 0 other;

Query Match 99.3%; Score 577.8; DB 20; Length 581;  
Best Local Similarity 99.7%; Pred. No. 2.9e-143;  
Matches 579; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGCGACCCAGCCTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTA 60  
QY 61 AGGCTGAGGCAGAAAGGTTATGTCTGTGAGAGTGGCCCTGGGAAAGGCCAGCCGCGAC 120  
DB 61 AAGCTGAGGCAGAAAGGTTATGTCTGTGAGAGTGGCCCTGGGAAAGGCCAGCCGCGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGTGAGAGACGAGTTTGAGACCCGTTTCCGCGCCACC 180  
DB 121 CCGCTGCACCAAGCCATGCGGGCTGTGTGAGAGACGAGTTTGAGACCCGTTTCCGCGCCACC 180  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAACGCTTCAAC 240  
DB 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAACGCTTCAAC 240  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCCTAACTGGGCGCTCTTTGGCATCTTT 300  
DB 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCCTAACTGGGCGCTCTTTGGCATCTTT 300  
QY 301 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA 360  
DB 301 GTCTTTGGGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGAGCCTTTGGTGGGA 360  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGGTGAATCCACAGC 420  
DB 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGGTGAATCCACAGC 420  
QY 421 AGTGGCGGCTGGGCGAGTTCACAGCTCTATACGGGACGCGGCCCTGGAGAGGCACGG 480  
DB 421 AGTGGCGGCTGGGCGAGTTCACAGCTCTATACGGGACGCGGCCCTGGAGAGGCACGG 480  
QY 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGGCACTG 540  
DB 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGGCACTG 540  
QY 541 GGGGCCCTGGTAACCTAGGGGCCCTTTTTCCTAGCAAGTG 581  
DB 541 GGGGCCCTGGTAACCTAGGGGCCCTTTTTCCTAGCAAGTG 581

RESULT 2  
AAT96578  
ID AAT96578 standard; DNA; 581 BP.  
XX  
AC AAT96578;

XX 22-APR-1998 (first entry)  
DT XX Mouse bcl-w DNA.  
DE XX  
XX Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
XW diagnosis; degenerative disease; ss.  
XX Mus sp.  
OS  
XX Key Location/Qualifiers  
FH 1..507  
FT /\*tag= a  
FT /product= bcl-w  
FT /note= "q"  
XX WC9735971-A1.  
PN 02-OCT-1997.  
XX 27-MAR-1997; 97WO-AU00199.  
XX 27-MAR-1996; 96AU-0008965.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.  
XX Adams JM, Cory S, Gibson LM, Holmgreen SP;  
P: WPI; 1997-489635/45.  
XX P-PSDB; AAW36048.  
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
PT or inhibit cell survival, e.g. for treatment of cancer and  
PT degenerative diseases  
XX Claim 3; Page 50-51; 86pp; English.  
PS This sequence encodes a novel gene, bcl-w, from the mouse bcl-2 gene  
XX family. This gene promotes cell survival, so its modulation is useful in  
CC treatment of cancer or auto-immune diseases, degenerative diseases (e.g.  
CC stroke, Alzheimer's disease, myocardial infarct, muscular degeneration,  
CC hypoxia, ischaemia, human immunodeficiency virus infection or in cell  
CC transplants. Up-regulation of the gene can also be used to modify cell  
CC lines cultured in vivo, e.g. to develop new lines, to facilitate  
CC isolation of hybridomas and to increase survival of primary explants  
CC during genetic modification. It can be used to produce recombinant Bcl-w  
CC for therapy, diagnosis, antibody production or screening of potential  
CC modulators.  
XX Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match 96.8%; Score 563.4; DB 18; Length 581;  
Best Local Similarity 98.1%; Pred. No. 1.9e-139;  
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
QY 1 ATGGGACCCAGCCTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 1 ATGGCGACCCAGCCTCAACCCAGACACAGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
QY 61 AGGCTGAGGCAGAAAGGTTATGTCTGTGAGAGTGGCCCTGGGAAAGGCCAGCCGCGAC 120  
DB 61 AGGCTGAGGCAGAAAGGTTATGTCTGTGAGAGTGGCCCTGGGAAAGGCCAGCCGCGAC 120  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGTGAGAGACGAGTTTGAGACCCGTTTCCGCGCCACC 180  
DB 121 CCGCTGCACCAAGCCATGCGGGCTGTGTGAGAGACGAGTTTGAGACCCGTTTCCGCGCCACC 180  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAACGCTTCAAC 240  
DB 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACACCCAGGCTCAGCCAGCAACGCTTCAAC 240  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCGCCTAACTGGGCGCTCTTTGGCATCTTT 300

Db 241 CAGGTTTCCGACGAACCTTTTCCAGGGGCCCCCTAACTGGGCGCTCTTGTGGCACTCTT 300  
Qy 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360  
Db 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360  
Qy 361 CAAGTGCAGGATGGATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTCCAGGATGGATCGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
Qy 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGACGGGCGCCCTGGAGGAGGACAGG 480  
Db 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGACGGGCGCCCTGGAGGAGGACAGG 480  
Qy 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCGCGTGGCACTG 540  
Db 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCGCGTGGCACTG 540  
Qy 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGCTAGCAAGTG 581  
Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGCTAGCAAGTG 581

RESULT 3  
AAX25135  
ID AAX25135 standard; DNA; 581 BP.  
XX  
AC AAX25135;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Mouse bcl-w gene derivative.  
XX  
KW Spermatogenesis; bcl-3 gene; Bcl-2; mouse; fertility; infertility;  
KW animal model; ss.  
XX  
OS Mus sp.

XX  
FH Key Location/Qualifiers  
FT CDS 1..507  
FT /\*tag= a  
XX  
PN WO9913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WO-AU00764.  
XX  
PR 16-SEP-1997; 97AU-C009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
XX

DR WPI; 1999-243890/20.  
DR P-PSDB; AAY05533.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w  
XX  
PS Disclosure; Page 38; 52pp; English.

XX  
CC The present sequence is described as a derivative of the mouse  
CC bcl-w gene (see AAX25133) and encodes Bcl-w protein (see AAY05533), a  
CC pro-survival member of the Bcl-2 family which is widely expressed  
CC and which is essential for spermatogenesis. The invention relates  
CC generally to a method of treatment and to an animal model for the  
CC identification of molecules and genetic sequences useful for  
CC inducing or reducing fertility of male animals. Methods are  
CC provided for the treatment of infertility, or for reducing  
CC fertility, by modulating spermatogenesis. An animal model carries  
CC a mutation is at least one allele of the human or murine bcl-w gene  
CC or in a gene associated with bcl-w. Such animals have disorganised

CC seminiferous tubules and are substantially infertile, but possess no  
CC other major abnormalities as determined by histological examination.  
CC They can be used to screen for therapeutic molecules including  
CC genetic sequences capable of inducing, enhancing or otherwise  
CC facilitating spermatogenesis in animals, or which can induce  
CC infertility.

XX  
SQ Sequence 581 BP; 105 A; 164 C; 195 G; 117 T; 0 other;

Query Match 96.8%; Score 563.4; DB 20; Length 581;  
Best Local Similarity 98.1%; Pred. No. 1.9e-139;  
Matches 570; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

Qy 1 ATGGCAGCCCCAGCCCTCAACCCCGACACACAGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGCCAGCCCCAGCCCTCAACCCCGACACACAGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Qy 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGGCCCTGGGGAAGCCCGCCGAC 120  
Db 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGGCCCTGGGGAAGCCCGCCGAC 120  
Qy 121 CCGCTGCACCAAGCCATGCGGCTGTGGAGACGAGTTTGAGACCCGTTTCCGCGCACC 180  
Db 121 CCGCTGCACCAAGCCATGCGGCTGTGGAGACGAGTTTGAGACCCGTTTCCGCGCACC 180  
Qy 181 TTCTCTGACCTGGCGCTCAGCTACACGTCAGCCAGGCTCAGCCAGCAAGCTTCACC 240  
Db 181 TTCTCTGACCTGGCGCTCAGCTACACGTCAGCCAGGCTCAGCCAGCAAGCTTCACC 240  
Qy 241 CAGGTTCCGACGAACTTTTCCAGGGGCCCTAACTGGGGCGCTCTTGTGGCATCTTT 300  
Db 241 CAGGTTCCGACGAACTTTTCCAGGGGCCCTAACTGGGGCGCTCTTGTGGCATCTTT 300  
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360  
Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360  
Qy 361 CAAGTGCAGGATGGATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTCCAGGATGGATCGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
Qy 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGACGGGCGCCCTGGAGGAGGACAGG 480  
Db 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGACGGGCGCCCTGGAGGAGGACAGG 480  
Qy 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCGCGTGGCACTG 540  
Db 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCGCGTGGCACTG 540  
Qy 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGCTAGCAAGTG 581  
Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGCTAGCAAGTG 581

RESULT 4  
AAV28333  
ID AAV28333 standard; cDNA; 579 BP.  
XX  
AC AAV28333;  
XX  
DT 02-OCT-1998 (first entry)  
XX  
DE Rat bcl-y gene.  
XX  
KW ss; bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.  
XX  
CS Rattus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..579  
FT /\*tag= a  
FT /product= bcl-y  
FT /note= "No stop codon given"





QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB |||||||  
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB |||||||  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGTGGCCCTGGGGAGGCCAGCCGCGGAC 120  
DB |||||||  
QY 61 AAGCTGAGACAGAGGGTTATGTCTGTGGAGTGGCCCTGGGGAGGCCAGCAGCCGAC 120  
DB |||||||  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGCTTTCCGCGCGCAC 180  
DB |||||||  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGCTTTCCGCGCGCAC 180  
DB |||||||  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB |||||||  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB |||||||  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCTAACTGGGGCCGCTTGTGGCATTCTTT 300  
DB |||||||  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCAACTGGGGCCGCTTGTGGCATTCTTT 300  
DB |||||||  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGGA 360  
DB |||||||  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGGA 360  
DB |||||||  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
DB |||||||  
QY 361 CAAGTGCAGGATTGGATGGTGGCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
DB |||||||  
QY 421 AGTGGCGCTGGCGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGAGGCGACGG 480  
DB |||||||  
QY 481 CGTCTGCGGGAGGGAACTGGGCACTCAGTGAACAGTCTGAGGACAGTCTGAGGAGGCTGTGGCACTG 540  
DB |||||||  
QY 481 CGTCTGCGGGAGGGAACTGGGCACTCAGTGAACAGTCTGAGGACAGTCTGAGGAGGCTGTGGCACTG 540  
DB |||||||

RESULT 6  
ABZ35729

ID ABZ35729 standard; DNA; 582 BP.  
XX  
AC ABZ35729;  
XX  
DT 07-FEB-2003 (first entry)  
XX  
DE Human bcl-w polynucleotide SEQ ID NO 37.  
XX

Double stranded RNA; dsRNA; RNAi; RNA inhibition; cyrostatic; virucide;  
KW protozoacide; gene expression; antisense; tumour; infection; Plasmodium;  
KW virus; viroid; anti-GFP; human; HIV; human immunodeficiency virus;  
KW Hepatitis C virus; human papilloma virus; gene; ds.

XX Homo sapiens.

XX DE10100588-A1.

PN 18-JUL-2002.

XX 09-JAN-2001; 2001DE-1000588.

XX 09-JAN-2001; 2001DE-1000589.

XX (R180-) RIBOPHARMA AG.

XX Kreutzer R, Limmer S, Rost S, Hadwiger P;

PI WPI; 2002-683450/74.

XX

PT Inhibiting expression of target genes, useful e.g. for treating tumors,  
PT by introducing into cells two double-stranded RNAs that are  
PT complementary to the target -  
XX  
PS Claim 13; Page 30-31; 100pp; German.  
XX  
CC The invention relates to inhibiting expression of a target gene in a cell  
CC by introducing at least two oligoribonucleotides (dsRNAI and II), both  
CC with a double-stranded (ds) structure of at most 49 sequential nucleotide  
CC pairs. At least part of one strand (S1, S2) of the ds structures in each  
CC of dsRNAI and II are complementary to regions in the target gene. The  
CC method uses antisense inhibition of gene expression using double stranded  
CC RNA inhibition (RNAi). The method is particularly used to treat tumours  
CC or infections, especially by Plasmodium or viruses/viroids (pathogenic on  
CC humans, animals or plants). The method provides more effective inhibition  
CC of expression than known methods using a single dsRNA, even at very low  
CC concentrations. When dsRNA has at least one unpaired nucleotide at the  
CC end, stability (and thus effective concentration in the cell) is  
CC improved and efficiency can be increased further by pretreating the cells  
CC with interferon. The present sequence is that of a target DNA of the  
CC invention.

XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match 90.1%; Score 524.4; DB 24; Length 582;  
Best Local Similarity 93.8%; Pred. No. 4e-129;  
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB |||||||  
QY 1 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
DB |||||||  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGTGGCCCTGGGGAGGCCAGCCGCGGAC 120  
DB |||||||  
QY 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGTGGCCCGGGAGGCCAGCAGCTGAC 120  
DB |||||||  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGCTTTCCGCGCGCAC 180  
DB |||||||  
QY 121 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCGCTTCGCGCGCAC 180  
DB |||||||  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB |||||||  
QY 181 TTCTCTGATCTGGCGGCTCAGTGCATGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB |||||||  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTTGTGGCATTCTTT 300  
DB |||||||  
QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTTCTTT 300  
DB |||||||  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGGA 360  
DB |||||||  
QY 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAAGAGATGGAGCCACTGGTGGGA 360  
DB |||||||  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
DB |||||||  
QY 361 CAAGTGCAGGAGTGGATGGTGGCCCTACCTGGAGACCGCGGCTGGCTGACTGGATCCACAGC 420  
DB |||||||  
QY 421 AGTGGCGGCTGGCGGAGTTTACAGCTCTATACGGGGACCGGGCCCTGGAGAGGCGACGG 480  
DB |||||||  
QY 421 AGTGGGGGCTGGGGGAGTTTACAGCTCTATACGGGGACCGGGCCCTGGAGAGGCGCGG 480  
DB |||||||  
QY 481 CGTCTGCGGGAGGGAACTGGGCACTCAGTGAACAGTCTGAGGAGCAGTCTGAGGAGGCTGTGGCACTG 540  
DB |||||||  
QY 481 CGTCTGCGGGAGGGAACTGGGCACTCAGTGAACAGTCTGAGGAGCAGTCTGAGGAGGCTGTGGCACTG 540  
DB |||||||

RESULT 7

ABX09972  
ID ABX09972 standard; DNA; 582 BP.  
XX

AC ABX09972;  
XX  
DT 23-JAN-2003 (first entry)  
XX  
DE Human bcl-w DNA fragment SEQ ID 37.  
XX  
KW Oligoribonucleotide; interferon; oncogene; cytokine; Id; developmental;  
KW prion; inhibition; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN DE10100587-Cl.  
XX  
XX  
PD 21-NOV-2002.  
XX  
PF 09-JAN-2001; 2001DE-1000587.  
XX  
PR 09-JAN-2001; 2001DE-1000587.  
XX  
XX (RIBO-) RIBOPHARMA AG.  
PA  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
XX WPI; 2002-742209/81.  
DR  
XX  
XX Inhibiting expression of target genes, e.g. oncogenes, in cells, by  
PT introduction of complementary double-stranded oligoribonucleotide,  
PT after treating the cell with interferon -  
XX  
XX  
PS Disclosure; Page 35-36; 98pp; German.  
XX  
XX This invention describes a novel method for inhibiting expression of a  
CC target gene by introducing into the cell that contains the target gene  
CC at least one oligoribonucleotide (dsRNA) that has a double-stranded  
CC (ds) structure of not more than 49 consecutive nucleotides (nt), where  
CC at least a segment of one strand of the ds structure is complementary  
CC with the target gene and the cells are treated with interferon before  
CC introduction of dsRNA. The method is used to inhibit expression of  
CC target genes, particularly oncogenes, cytokine genes, Id (not defined);  
CC protein genes; developmental or prion genes, or genes expressed in  
CC pathogenic organisms (particularly plasmodia) or in viruses or viroids  
CC (pathogenic in humans, animals or plants). Treating the cells with  
CC interferon greatly increases the extent to which dsRNA can inhibit  
CC expression of the target genes, and the effect is even greater when dsRNA  
CC are modified to increase their stability. ABX09936-ABX10075 represent  
CC gene fragments used to illustrate the method of the invention.  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match 90.1%; Score 524.4; DB 24; Length 582;  
Best Local Similarity 93.8%; Pred. No. 4e-129;  
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCAGACACACACCGGCTCTAGTGGTGAATTTGTAGGCTAT 60  
DB |||||  
1 ATGGCGACCCAGCCTCGGCCAGACACACACCGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
QY 61 AGGCTGAGGCAGAGGGTTATGCTCTGGAGCTGGCCCTGGGGAGAGCCCGGCGAC 120  
DB |||||  
61 AAGCTGAGGCAGAGGGTTATGCTCTGGAGCTGGCCCGGGAGAGCCCGGCGAGCTGAC 120  
QY 121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGACGAGTTTGAGACCCGTTTCCGCGCACC 180  
DB |||||  
121 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCCGCTTCCGCGCACC 180  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
DB |||||  
181 TTCTCTGATCTGGCGGCTCAGCTGCAATGACCCAGGCTCAGCCAGCAACGCTTCACC 240  
QY 241 CAGGTTTCCGACGAACCTTTTCAAGGGGCGCCCTAACTGGGGCCGCTTGTGGCATCTTT 300  
DB |||||  
241 CAGGTTTCCGACGAACCTTTTCAAGGGGCGCCCAACTGGGGCCGCTTGTAGCCTCTTT 300

QY 301 GTCTTTGGGGTCCCTGTGTGTGCTGAGAGTGTCAACAAAGAAATGAGCCCTTTGGTGGGA 360  
DB |||||  
301 GTCTTTGGGGTGCACACTGTGTGCTGAGAGTGTCAACAAAGAGATGAACCACTGGTGGGA 360  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
DB |||||  
361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACCGGGCTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGCGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGCGG 480  
DB |||||  
421 AGTGGCGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGCGCGG 480  
QY 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCCTGGGCACTG 540  
DB |||||  
481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCCTGGGCACTG 540  
QY 541 GGGGGCCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGA 582  
DB |||||  
541 GGGGGCCCTGGTAACTGTAGGGGCCCTTTTGTGCTAGCAAGTGA 582

RESULT 8  
ABV78153  
ID ABV78153 standard; DNA; 582 BP.  
XX  
AC ABV78153;  
XX  
DT 15-NOV-2002 (first entry)  
XX  
DE Human bcl-w DNA SEQ ID NO 37.  
XX  
KW RNA inhibition; dsRNA; gene expression inhibitor; oncogene; cytostatic;  
KW virucide; protozoacide; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200255693-A2.  
XX  
PD 18-JUL-2002.  
XX  
PF 09-JAN-2002; 2002WO-EP00152.  
XX  
PR 09-JAN-2001; 2001DE-1000586.  
PR 26-OCT-2001; 2001DE-1055280.  
PR 29-NOV-2001; 2001DE-1058411.  
PR 07-DEC-2001; 2001DE-1060151.  
XX  
PA (RIBO-) RIBOPHARMA AG.  
XX  
PI Kreutzer R, Limmer S, Rost S, Hadwiger P;  
XX  
XX WPI; 2002-590671/63.  
DR  
XX  
PT Inhibiting expression of target gene, useful e.g. for inhibiting  
PT oncogenes, by administering double-stranded RNA complementary to the  
PT target and having an overhang -  
XX  
XX Claim 10; Page 134; 203pp; German.  
XX  
XX The invention relates to inhibiting expression of a target gene (I) in a  
CC cell by introducing an inhibitory RNA (dsRNA) having a double-stranded  
CC structure of at most 49 consecutive bases. At least part of one strand  
CC (as1) of dsRNA is complementary to (I) and at least one end of dsRNA  
CC has an overhang of 1-4 nucleotides. The method is used to inhibit the  
CC expression of a wide range of genes, e.g. oncogenes, cytokine genes etc.  
CC in humans, also genes in Plasmodium or in viruses or viroids that are  
CC pathogenic for humans, animals or plants. Introducing an overhang into  
CC dsRNA greatly increases effectiveness for inhibiting gene expression,  
CC both in vivo and in vitro and also increases stability and thus the  
CC effective concentration inside the cell. The present sequence is that of  
CC a gene related to the invention.  
XX  
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

```
Query Match          90.1%; Score 524.4; DB 24; Length 582;
Best Local Similarity 93.8%; Pred. No. 4e-129;
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCCTCAACCCCGAGACACACCGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
    |||||
Db 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACCGGGCTCTGGTGGCAGACTTTGTAGGCTAT 60

QY 61 AGGTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120
    |||||
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGGGCGCTGCTGGAGACGAGTTTGAGACCCGCTTCCGCGGAC 180
    |||||
Db 121 CCGCTGCACCAAGCCATGGCGGCGAGCTGGAGATGAGTTCGAGACCCGCTTCCGCGGAC 180

QY 181 TTCTCTGACCTGGCGGCTCAGCTACAGGTGACCCCGAGGCTCAGCCCGAGAACGCTTCAC 240
    |||||
Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCCGAGGCTCAGCCCGAGAACGCTTCAC 240

QY 241 CAGGTTCCGACGAACCTTTCCAGGGGGCCCTAACTGGGCGCTCTGTGGCATTCCTT 300
    |||||
Db 241 CAGGTTCCGACGAACCTTTTCAAGGGGGCCCACTGGGCGCCCTTGTAGCCTTCCTT 300

QY 301 GTCTTTGGGGCTGCCCTGTCTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360
    |||||
Db 301 GTCTTTGGGGCTGCCCTGTCTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360

QY 361 CAAGTCAGGATTGGATGGTGGCCCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
    |||||
Db 361 CAAGTCAGGAGTGGATGGTGGCCCTACCTGGAGACAGCGGCTGGCTGACTGGATCCACAGC 420

QY 421 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCGG 480
    |||||
Db 421 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGAGTGTGACGGGGCCCTGGCACTG 540

QY 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
    |||||
Db 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
```

```
RESULT 9
ABL91694
ID ABL91694 standard; DNA; 582 BP.
XX
AC ABL91694;
XX
DT 28-MAY-2002 (first entry)
XX
DE Human polynucleotide SEQ ID NO 37.
XX
KW Human; HIV; HCV; gene expression; oligoribonucleotide; tumour; pathogen;
KW Plasmodium; virus; viroid; cytokine; prion; antisense oligonucleotide;
KW cytostatic; virucide; protozoacide; antibacterial; ds.
XX
OS Homo sapiens.
XX
PN DE10100586-C1.
XX
PD 11-APR-2002.
XX
PF 09-JAN-2001; 2001DE-1000586.
XX
PR 09-JAN-2001; 2001DE-1000586.
XX
PA (RIBO-) RIBOPHARMA AG.
XX
PI Kreutzer R, Zimmer S, Rost S, Hadwiger P;
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XX WPI; 2002-270454/32.
XX
PT inhibiting gene expression in cells, useful for e.g. treating tumors,
PT by introducing double-stranded complementary oligoRNA having unpaired
PT terminal bases -
XX
PS Claim 13; Page 32; 104pp; German.
XX
CC The invention relates to a method for inhibiting expression of a target
CC gene (ABL91658-ABL91797) in a cell by introducing at least one
CC oligoribonucleotide that has a double-stranded structure consisting of at
CC most 49 sequential nucleotide pairs, with at least part of one strand
CC complementary with the target gene and has at least one end a
CC single-stranded segment of 1-4 nt. The method provides
CC oligoribonucleotides for antisense inhibition of gene expression useful
CC e.g. for treating tumours but the oligoribonucleotides may also be
CC directed against genes present in pathogens (e.g. Plasmodium or
CC viruses/viroids, pathogenic on humans, animals or plants) or against
CC cytokine, Id, developmental or prion genes. The method provides more
CC effective inhibition of gene expression than use of known
CC oligonucleotides, probably because the unpaired overhang increases
CC stability and thus intracellular concentration.
XX
SQ Sequence 582 BP; 104 A; 156 C; 211 G; 111 T; 0 other;

Query Match          90.1%; Score 524.4; DB 24; Length 582;
Best Local Similarity 93.8%; Pred. No. 4e-129;
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCCTCAACCCCGAGACACACCGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
    |||||
Db 1 ATGGCGACCCAGCCCTCGGCCCCAGACACACCGGGCTCTGTGGCAGACTTTGTAGGCTAT 60

QY 61 AGGTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120
    |||||
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGGCGGCTGCTGGAGACGAGTTTGAGACCCGCTTCCGCGGAC 180
    |||||
Db 121 CCGCTGCACCAAGCCATGGCGGCGAGTGTGCTGAGAGTGTGACGGGCGCTTCCGCGGAC 180

QY 181 TTCTCTGACCTGGCGGCTCAGCTACAGGTGACCCCGAGGCTCAGCCCGAGAACGCTTCAC 240
    |||||
Db 181 TTCTCTGATCTGGCGGCTCAGCTGATGTGACCCCGAGGCTTCCGCGGCGAC 240

QY 241 CAGGTTCCGACGAACCTTTTCCAGGGGGCCCTAACTGGGCGCTCTGTGGCATTCCTT 300
    |||||
Db 241 CAGGTTCCGACGAACCTTTTCAAGGGGGCCCACTGGGCGCCCTTGTAGCCTTCCTT 300

QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360
    |||||
Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360

QY 361 CAAGTCAGGATTGGATGGTGGCCCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
    |||||
Db 361 CAAGTCAGGAGTGGATGGTGGCCCTACCTGGAGACAGCGGCTGGCTGACTGGATCCACAGC 420

QY 421 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCGG 480
    |||||
Db 421 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGAGTGTGACGGGGCCCTGGCACTG 480

QY 481 CGTCTCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGCACTG 540
    |||||
Db 481 CGTCTCGGGAGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGCACTG 540

QY 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
    |||||
Db 541 GGGGCCCTGGTAAGTGTAGGGGCTTTTGTGCTAGCAAGTGA 582
```

RESULT 10  
ABL16642



ID ABT16642 standard; DNA; 3542 BP.  
XX  
AC ABT16642;  
XX  
DT 03-APR-2003 (first entry)  
XX  
DE Human bcl-2 gene SEQ ID No 4.  
XX  
KW Anti-tumour; DNzyme; bcl-2 gene; tumour; malignant; chemotherapy;  
KW radiation therapy; catalytic domain; enzyme; human; ds.  
XX  
OS Homo sapiens.  
XX  
PN W020029090-A1.  
XX  
PD 12-DEC-2002.  
XX  
PF 07-JUN-2002; 2002WO-AU00739.  
XX  
PR 07-JUN-2001; 2001AU-0005527.  
XX  
PA (JOHJ ) JOHNSON & JOHNSON RES PTY LTD.  
XX  
PI Sun L, Wang L, Turner RJ, Saravolac EG, Dass CR;  
XX  
DR WPI; 2003-140617/13.  
XX  
XX Novel DNzyme useful for treating tumors, and for enhancing the  
PT sensitivity of malignant or virus infected cells to therapy, comprises  
PT a catalytic domain and binding domain contiguous to the catalytic  
PT domain -  
XX  
PS Disclosure; Page 44-45; 67pp; English.  
XX  
XX The invention relates to a DNzyme which specifically cleaves mRNA  
CC transcribed from a member of the bcl-2 gene family. The DNzymes comprise  
CC a catalytic domain, binding domains contiguous with the 5' and 3' end of  
CC the catalytic domain, and therefore hybridise with, the two regions  
CC immediately flanking the purine residue of the cleavage site within the  
CC bcl-2 gene family mRNA, at which DNzyme-catalysed cleavage is desired. A  
CC pharmaceutical composition comprising a DNzyme of the invention is  
CC useful for treating tumours in a subject, and for enhancing the  
CC sensitivity of malignant or virus infected cells infected cells to  
CC therapy. The DNzymes are useful in diagnostics, therapeutics,  
CC prophylaxis, research agents and in kits. The DNzymes are also  
CC useful for increasing the susceptibility of tumour cells to anti-tumour  
CC therapies such as chemotherapy and radiation therapy. This polynucleotide  
CC sequence represents a human bcl-2 gene of the invention.  
XX  
SQ Sequence 3542 BP; 804 A; 817 C; 1030 G; 891 T; 0 other;  
  
Query Match 89.6%; Score 521.2; DB 25; Length 3542;  
Best Local Similarity 93.5%; Pred. No. 4.7e-128;  
Matches 544; Conservative 0; Mismatches 38; Indels 0; Gaps 0;  
  
QY 1 ATGGCGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db |||||  
177 ATGGCGACCCAGCCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 236  
  
QY 61 AGGCTGAGGCGAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120  
Db |||||  
237 AAGCTGAGGCGAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 296  
  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTTCGCGGCACC 180  
Db |||||  
297 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTGAGACCCGCTTCGCGGCACC 356  
  
QY 181 TTCTCTGACCTGGCGGCTCAGCTACAGTACCCAGCTCAGCCAGCAACGTTTACC 240  
Db |||||  
357 TTCTCTGATCTGGCGGCTCAGCTGTCATGTGACCCAGGCTCAGCCCAACACGTTTACC 416  
  
QY 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCTAACTGGGCGCTCTTGTGGATTCTTT 300  
Db |||||

Db 417 CAGGTCTCCGATGAACCTTTTTCAGAGGGGGCCCCAACCTGGGGCCGCTTGTAGCCTTCTTT 476  
QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGGA 360  
Db 477 GTCTTTGGGCTGCACACTGTGTGCTGAGAGTGTCAACAAAGGAGATGGAACCACTGGTGGGA 536  
QY 361 CAAGTGCAGGATTGGATGGTGGCTACCTGGAGACACGCTGGCTGACTGGATCCACAGC 420  
Db 537 CAAGTGCAGGAGTGGATGGTGGCTACCTGGAGACGCGGCTGGCTGACTGGATCCACAGC 596  
QY 421 AGTGGCGGCTGGGCGGAGTTTACAGCTCTATACGGGACGGGGCCCTGGAGAGGACACGG 480  
Db 597 AGTGGGGCTGGGCGGAGTTTACAGCTCTATACGGGACGGGGCCCTGGAGAGGACGCGGG 656  
QY 481 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGGCACTG 540  
Db 657 CGTCTGCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCCCTGGGCACTG 716  
QY 541 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 582  
Db 717 GGGGCCCTGGTAACTGTAGGGGCGCTTTTGTCTAGCAAGTGA 758  
  
RESULT 11  
AAAX25132  
ID AAX25132 standard; DNA; 581 BP.  
XX  
AC AAX25132;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human bcl-w gene.  
XX  
KW Spermatogenesis; bcl-3 gene; Bcl-2; human; fertility; infertility;  
KW animal model; ss.  
OS Homo sapiens.  
XX  
PN W09913710-A1.  
XX  
PD 25-MAR-1999.  
XX  
PF 16-SEP-1998; 98WC-AU00764.  
XX  
PR 16-SEP-1997; 97AU-0009228.  
XX  
PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX  
PI Adams J, Cory S, Gibson J, Koentgen F, Print C;  
XX  
DR WPI; 1999-243890/20.  
DR P-PSDB; AAY05530.  
XX  
PT An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w  
XX  
PS Claim 3; Page 32; 52pp; English.  
XX  
CC The present sequence is the human bcl-w gene encoding Bcl-w protein  
CC (see AAY05530), a pro-survival member of the Bcl-2 family which is  
CC widely expressed and which is essential for spermatogenesis. The  
CC invention relates generally to a method of treatment and to an  
CC animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male  
CC animals. Methods are provided for the treatment of infertility, or  
CC for reducing fertility, by modulating spermatogenesis. An animal  
CC model carries a mutation is at least one allele of the human or  
CC murine bcl-w gene or in a gene associated with bcl-w. Such animals  
CC have disorganised seminiferous tubules and are substantially  
CC infertile, but possess no other major abnormalities as determined  
CC by histological examination. They can be used to screen for  
CC therapeutic molecules including genetic sequences capable of  
CC inducing, enhancing or otherwise facilitating spermatogenesis in

```
CC animals, or which can induce infertility.
SQ Sequence 581 BP; 104 A; 155 C; 210 G; 112 T; 0 other;

Query Match      89.4%; Score 520.2; DB 20; Length 581;
Best Local Similarity 93.3%; Pred. No. 5.1e-128;
Matches 543; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGGGACCCAGCCTCAACCCAGACACACAGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGGACCCAGCCTCGGCCAGACACACAGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGGCCAGCAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGCTGCTGGAGACGAGTTTGAGACCCGCTTCCGCGGCACC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCGCTTCCGCGGCACC 180

QY 181 TTCTCTGATCTGGCGCTCAGTGCATGTGACCCAGGCTCAGCCCAACAAACGCTTCACC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTCTCTGATCTGGCGCTCAGTGCATGTGACCCAGGCTCAGCCCAACAAACGCTTCACC 240

QY 241 CAGGTTCCGACGAACCTTTTCAAGGGGCGCCCTAAGTGGGCGCTCTTTGGCATTCTTT 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CAGGTTCCGATGAACCTTTTCAAGGGGCGCCCAACTGGGCGCGCTTTGAGCCTTCTTT 300

QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGTTGGGA 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGAGATGGAACCACTGTTGGGA 360

QY 361 CAAAGTCAGGATTTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGATCCACAGC 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CAAAGTCAGGATTTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGATCCACAGC 420

QY 421 AGTGGCGCTGGCGGAGTTTCAAGGAGTTCACAGCTCTATACGGGACGGGCGCTTGGAGAGCGG 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 AGTGGCGCTGGCGGAGTTTCAAGGAGTTCACAGCTCTATACGGGACGGGCGCTTGGAGAGCGG 480

QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGGCACTG 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGGCACTG 540
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RESULT 12
AAT96577
ID AAT96577 standard; DNA; 583 BP.
AC AAT96577;
XX
DT 22-APR-1998 (first entry)
XX
DE Human bcl-w DNA.
XX
KW Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;
KW diagnosis; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 1..582
FT /*tag= a
FT /product= bcl-w
XX
PN W09735971-A1.
XX
PD 02-OCT-1997.
XX
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PF 27-MAR-1997; 97WO-AU00199.
XX
PR 27-MAR-1996; 96AU-0008965.
XX
PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
PI Adams JM, Cory S, Gibson LM, Holmgren SP;
XX
DR WPI; 1997-489635/45.
DR P-PSDB; AAW36047.
XX
PT Nucleic acid encoding apoptosis related gene bcl-w - used to induce
PT or inhibit cell survival, e.g. for treatment of cancer and
PT degenerative diseases
XX
PS Claim 3; Page 48; 86pp; English.
XX
XX This sequence encodes a novel human gene, bcl-w, from the bcl-2 gene
XX family, extracted from an adult brain library. This gene promotes cell
XX survival, so its modulation is useful in treatment of cancer or
XX auto-immune diseases, degenerative diseases (e.g. stroke, Alzheimer's
XX disease, myocardial infarct, muscular degeneration, hypoxia, ischaemia,
XX human immunodeficiency virus infection or in cell transplants.
XX Up-regulation of the gene can also be used to modify cell lines cultured
XX in vivo, e.g. to develop new lines, to facilitate isolation of hybridomas
XX and to increase survival of primary explants during genetic modification.
XX It can be used to produce recombinant Bcl-w for therapy, diagnosis,
XX antibody production or screening of potential modulators.
SQ Sequence 583 BP; 105 A; 157 C; 210 G; 111 T; 0 other;

Query Match      89.3%; Score 519.6; DB 18; Length 583;
Best Local Similarity 93.3%; Pred. No. 7.4e-128;
Matches 543; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCAGACACAGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGCGACCCAGCCTCGGCCAGACACACAGGCTCTGGTGGCAGACTTTGTAGGTTAT 60

QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGGCCAGCAGCTGAC 120
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGGCCAGCAGCTGAC 120

QY 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCGCTTCCGCGGCACC 180
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGAGTTGAGACCCGCTTCCGCGGCACC 180

QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTCAGCCACCCAGGCTCAGCCCAACAGCTTCACC 240
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACAGCTTCACC 240

QY 241 CAGGTTTCCGACGAACCTTTTCAAGGGGCGCCCTAAGTGGGCGCTTGTGGCACTCTTT 300
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 241 CAGGTTTCCGACGAACCTTTTCAAGGGGCGCCCAACTGGGCGCGCTTGTAGCCTTCTTT 300

QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGTTGGGA 360
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGTTGGGA 360

QY 361 CAAAGTCAGGATTTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGATCCACAGC 420
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 CAAAGTCAGGATTTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGATCCACAGC 420

QY 421 AGTGGCGCTGGCGGAGTTTCAAGGAGTTCACAGCTCTATACGGGACGGGCGCTTGGAGAGCGG 480
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 AGTGGCGCTGGCGGAGTTTCAAGGAGTTCACAGCTCTATACGGGACGGGCGCTTGGAGAGCGG 480

QY 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGGCACTG 540
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 CGTCTCGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGCTGGGCACTG 540

QY 541 GGGGCGCTGGTAACTGTAGGGGCGCTTTTGTGCTAGCAAGTG 582
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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CC family, components in the cell death pathway. The bcl-2 family  
CC have both apoptotic activity and the apoptosis blocking activity. bcl-y  
CC falls in the apoptosis activity category. The recombinant protein may  
CC be used to prevent uncontrolled cell growth, either by its direct  
CC administration to recombinant genetic constructs to increase its  
CC expression in vivo. Also, antisense constructs can be used in disorders  
CC where prevention of cell death is desired.  
XX  
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match: 88.5%; Score 515; DB 19; Length 579;  
Best Local Similarity 93.1%; Pred. No. 1.2e-126;  
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCAGACACACAGGGCTCTAGTGGTGAAGCTTTGTAGGCTAT 60  
Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
1 ATGGCGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGGTGAAGACTTTGTAGGTTAT 60  
  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCCGCGAC 120  
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121 CCACTGCACCAAGCCATCGGGCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 180  
  
QY 181 TTCTCTGACCTGGCGCTCAGCTACACGTCAGCCCCAGGCTCAGCCAGCAACGCTTCACC 240  
Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
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QY 301 GTCTTTGGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAAATGAGCCCTTTGGTGGGA 360  
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361 CAAGTGCAGGATGGATGGTGGCTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420  
  
QY 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480  
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QY 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGCTGGCACTG 540  
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QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTTCGTAGCAAG 579  
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RESULT 15  
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ID AAX15946 standard; cDNA; 579 BP.  
XX  
AC AAX15946;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE cDNA encoding the human bcl-y protein.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite; ss.

XX Homo sapiens.  
XX  
XX JS5863229-A.  
XX  
XX 16-MAR-1999.  
XX  
XX 25-NOV-1997; 97US-0978523.  
XX  
XX 23-FEB-1996; 96US-C012201.  
XX 11-FEB-1997; 97US-0798897.  
XX 25-NOV-1997; 97US-0978523.  
XX  
XX (COCE-) COCENSYS INC.  
XX  
XX Guastella J;  
XX  
XX WPI; 1999-214150/i8.  
XX P-PSDB; AAW97392.  
XX  
XX Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
XX for modulating programmed cell death  
XX  
XX Disclosure; Columns 15-16; 26pp; English.  
XX  
XX The present sequence encodes human bcl-y protein (Hbcl-y). The  
XX specification also describes rat bcl-y protein (Rbcl-y). Rbcl-y and  
XX Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
XX programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
XX proteins may be used to treat conditions associated with a disruption of  
XX the cell death pathway. If they act as cell death inhibitors, they may be  
XX used in therapies to treat subjects suffering from: strokes, head trauma,  
XX Alzheimer's Disease, neural and muscular degenerative diseases  
XX (especially multiple sclerosis), myocardial infarction, vitally induced  
XX cell death, aging, spinal cord injuries and amyotrophic lateral  
XX sclerosis- conditions where cells under go premature cell death as a  
XX result of triggers which may or may not be apparent. They may also be  
XX used in this way to develop cell lines which remain viable in culture for  
XX an extended period. In contrast, if they act as cell death stimulators,  
XX Rbcl-y and Hbcl-y may be used to treat conditions associated with  
XX prolonged cell life span such as cancer (especially kaposi's sarcoma and  
XX lung cancer) and auto/hyperimmune diseases. They may also be used to  
XX cause cell death in, and hence control, parasites.  
XX  
SQ Sequence 579 BP; 106 A; 154 C; 208 G; 111 T; 0 other;

Query Match 88.5%; Score 515; DB 20; Length 579;  
Best Local Similarity 93.1%; Pred. No. 1.2e-126;  
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCAGACACACAGGGCTCTAGTGGTGAAGCTTTGTAGGCTAT 60  
Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
1 ATGGCGACCCAGCCTCGGCCCCAGACACACAGGGCTCTGGTGAAGACTTTGTAGGTTAT 60  
  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCCGCGAC 120  
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QY 241 CAGGTTCCGACGAACCTTTTCCAAGGGGCCCTAACTGGGGCGCTTGTGGCATTTCTTT 300  
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QY 301 GTCTTTGGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAAATGAGCCCTTTGGTGGGA 360  
Db |||||||||||| |||||||||||| |||||||||||| |||||||||||| ||||||||||||  
301 GTCTTTGGGCTGCACTGTGTCTGAGAGTGTCAACAAGGATGGAACCACTGGTGGGA 360



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Db			
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Qy	421	AGTGGGGCTGGGCGGAGTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG	480
Db			
Qy	481	CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCCTGGGCACTG	540
Db			
Qy	481	CGTCTGCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCCTGGGCACTG	540
Db			
Qy	541	GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG	579
Db			
Qy	541	GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG	579
Db			

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OMnucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:53:10 ; Search time 43.4627 Seconds  
(without alignments)  
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Perfect score: 582  
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Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents NA:\*

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6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	558.2	95.9	579	1 US-08-798-897-1	Sequence 1, Appli
2	558.2	95.9	579	2 US-08-978-523-1	Sequence 1, Appli
3	515	88.5	579	1 US-08-798-897-2	Sequence 2, Appli
4	515	88.5	579	2 US-08-978-523-2	Sequence 2, Appli
5	372.4	64.0	1864	4 US-09-149-476-130	Sequence 130, App
6	134.6	23.1	926	1 US-08-081-448-5	Sequence 5, Appli
7	134.6	23.1	926	2 US-08-470-670A-6	Sequence 6, Appli
8	134.6	23.1	926	3 US-08-481-739-1	Sequence 1, Appli
9	134.6	23.1	926	3 US-09-167-921-1	Sequence 1, Appli
10	134.6	23.1	926	3 US-09-277-020-39	Sequence 39, Appl
11	134.6	23.1	926	3 US-09-323-743-1	Sequence 1, Appli
12	134.6	23.1	926	4 US-08-461-511A-6	Sequence 6, Appli
13	134.6	23.1	926	4 US-09-271-014A-5	Sequence 5, Appli
14	134.6	23.1	926	5 PCT-US94-07089-6	Sequence 6, Appli
15	121.8	20.9	717	2 US-08-465-485A-20	Sequence 20, Appl
16	121.8	20.9	717	3 US-09-080-285-20	Sequence 20, Appl
17	121.8	20.9	1274	2 US-08-470-670A-1	Sequence 1, Appli
18	121.8	20.9	1274	4 US-08-461-511A-1	Sequence 1, Appli
19	121.8	20.9	1274	5 PCT-US94-07089-1	Sequence 1, Appli
20	121.8	20.9	1303	1 US-08-081-448-1	Sequence 1, Appli
21	121.8	20.9	1303	4 US-09-271-014A-1	Sequence 1, Appli
22	121.8	20.9	4825	6 5459251-1	Patent No. 5459251
23	121.8	20.9	5086	2 US-08-465-485A-19	Sequence 19, Appl
24	121.8	20.9	5086	2 US-08-365-486A-14	Sequence 14, Appl
25	121.8	20.9	5086	3 US-09-080-285-19	Sequence 19, Appl
26	121.8	20.9	5086	3 US-08-880-342-14	Sequence 14, Appl
27	121.8	20.9	5086	4 US-09-724-426-19	Sequence 19, Appli

28	121.8	20.9	5086	4 US-09-233-527-7	Sequence 7, Appli
29	121.8	20.9	5086	5 PCT-US93-05651-4	Sequence 4, Appli
30	121.8	20.9	5086	5 PCT-US93-06251-2	Sequence 2, Appli
31	121.8	20.9	5094	4 US-09-234-186-7	Sequence 7, Appli
32	121.8	20.9	5104	6 5506344-1	Patent No. 5506344
33	120.2	20.7	760	1 US-08-405-702A-11	Sequence 11, Appl
34	120.2	20.7	1846	2 US-08-365-486A-16	Sequence 16, Appl
35	120.2	20.7	1846	3 US-08-880-342-16	Sequence 16, Appl
36	117.4	20.2	615	2 US-08-465-485A-22	Sequence 22, Appl
37	117.4	20.2	615	3 US-09-080-285-22	Sequence 22, Appl
38	117.4	20.2	911	3 US-09-126-109-5	Sequence 5, Appli
39	117.4	20.2	911	5 PCT-US93-06251-3	Sequence 3, Appli
40	115.6	19.9	1384	4 US-08-899-367-1	Sequence 1, Appli
41	114.2	19.6	831	6 5459251-3	Patent No. 5459251
42	114.2	19.6	831	6 5506344-4	Patent No. 5506344
43	73.2	12.6	623	6 5506344-3	Patent No. 5506344
44	57	9.8	737	1 US-08-081-448-7	Sequence 7, Appli
45	57	9.8	737	2 US-08-470-670A-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
US-08-798-897-1  
; Sequence 1, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20035  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 579 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; MOLECULE TYPE: cDNA  
US-08-798-897-1

Query Match: 95.9%; Score 558.2; DB 1; Length 579;  
Best Local Similarity 97.8%; Pred. No. 4.9e-143;  
Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY	1	ATGGCGACCCCGCCTCAACCCCGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT	60
Dd	1	ATGGCGACCCCGCCTCAACCCCGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT	60
QY	61	AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGAAGCCCGCCGAC	120

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Db 61 AAGCTGAGACAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGAAAGGCCACAGCCGAC 120
QY 121 CCGCTGCACCAAGCCATGCGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCGGCACC 180
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QY 361 CAAGTGCAGGATTGGATGTGGCCCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
Db 361 CAAGTGCAGGATTGGATGTGGACCTACCTGGAGACAGCTCTGGCTGACTGGATCCACAGC 420
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Db 421 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGCCCTGGAGAGGCACGG 480
QY 481 CGTCTCGGGAGGGGAACTGGGCATCAGTGAGGACAGTGTGACGGGGCGTGGCACTG 540
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Db 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579
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RESULT 2

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US-08-978-523-1
; Sequence 1, Application US/08978523
; Patent No. 5883229
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/978,523
; FILING DATE: herewith
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/798,897
; FILING DATE: February 11, 1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmord, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1483.0140002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 1:
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-08-978-523-1

Query Match 95.9%; Score 558.2; DB 2; Length 579;
Best Local Similarity 97.8%; Pred. No. 4.9e-143;
Matches 566; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCCTCAACCCCGAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db 1 ATGGCGACCCAGCCCTCAACCCCGAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGAAAGGCCCGCCGAC 120
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QY 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579
Db 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTGTGCTAGCAAG 579
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RESULT 3

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US-08-798-897-2
; Sequence 2, Application US/08798897
; Patent No. 5789201
; GENERAL INFORMATION:
; APPLICANT: Guastella, John
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2
; TITLE OF INVENTION: Homologue
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 New York Avenue, N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-08-798-897-2

Query Match 88.5%; Score 515; DB 1; Length 579;  
Best Local Similarity 93.1%; Pred. No. 2.9e-131;  
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCAACCCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGGCGACCCAGCCTCGGCCCGAGACACACGGGCTCTGGTGAAGACTTTGTAGGTTAT 60  
QY 61 AGGCTGAGGCAGAGGGTTATGCTGTGAGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120  
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Db 361 CAAGTGCAGGATGGATGGTGGCCCTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGAGTTTACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCACGG 480  
Db 421 AGTGGCGGCTGGCGGAGTTTACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCAGG 480  
QY 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCCGCTGGCACTG 540  
Db 481 CGTCTCGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGACGGGGCCGCTGGCACTG 540  
QY 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGTAGCAAG 579  
Db 541 GGGGCCCTGGTAAGTGTAGGGGCCCTTTTGTGTAGCAAG 579

RESULT 4  
US-08-978-523-2  
Sequence 2, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2

TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 579 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
MOLECULE TYPE: cDNA  
US-08-978-523-2

Query Match 88.5%; Score 515; DB 2; Length 579;  
Best Local Similarity 93.1%; Pred. No. 2.9e-131;  
Matches 539; Conservative 0; Mismatches 40; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCAACCCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGGCGACCCAGCCTCGGCCCGAGACACACGGGCTCTGGTGAAGACTTTGTAGGTTAT 60  
QY 61 AGGCTGAGGCAGAGGGTTATGCTGTGAGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120  
Db 61 AAGCTGAGGCAGAGGGTTATGCTGTGAGAGCTGGCCCTGGGGAAGGCCAGCGTGC 120  
QY 121 CCGCTGCACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCGCTTCCGCCGAC 180  
Db 121 CCACTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGCGGACC 180  
QY 181 TTCTCTGACCTGGCGCTCAGCTACACGTACACCCCGAGGCTCAGCCGCAACGCTTCACC 240  
Db 181 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCCGAGGCTCAGCCCAACGCTTCACC 240  
QY 241 CAGGTTTCCGAGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGCTTGTGGCATCTTT 300  
Db 241 CAGGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTCTTT 300  
QY 301 GTCTTTGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360  
Db 301 GTCTTTGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACCGTCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGATGGATGGTGGCCCTACCTGGAGACCGGCTGGCTGACTGGATCCACAGC 420  
QY 421 AGTGGCGGCTGGCGGAGTTTACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCACGG 480  
Db 421 AGTGGCGGCTGGCGGAGTTTACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCAGG 480



QY 481 CGTCTGGGAGGGGAAGTGGGCATCACTGAGGACAGTGTGACGGGGCGGTGGCACTG 540  
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481 CGTCTGGGAGGGGAAGTGGGCATCACTGAGGACAGTGTGACGGGGCGGTGGCACTG 540  
QY 541 GGGGCCCTGGTAAGTGTAGGGCCCTTTTGTCTAGCAAG 579  
Dd [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||] [|||||]  
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RESULT 5

US-09-149-476-130  
; Sequence 130, Application US/09149476  
; Patent No. 6420526  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P1  
; CURRENT APPLICATION NUMBER: US/09/149,476  
; CURRENT FILING DATE: 1998-09-08  
; EARLIER APPLICATION NUMBER: PCT/US98/04493  
; EARLIER FILING DATE: 1998-03-06  
; EARLIER APPLICATION NUMBER: 60/040,162  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/040,333  
; EARLIER FILING DATE: 1997-03-07  
; EARLIER APPLICATION NUMBER: 60/038,621  
; EARLIER FILING DATE: 1997-03-07  
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; EARLIER APPLICATION NUMBER: 60/047,600  
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; EARLIER APPLICATION NUMBER: 60/047,615  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,597  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,502  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,633  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,617  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,618  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,503  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,584  
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; EARLIER APPLICATION NUMBER: 60/047,500  
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; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596

; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
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; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
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; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
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; EARLIER APPLICATION NUMBER: 60/056,874  
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; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22

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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
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EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,909  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,862  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02

Query Match 64.0%; Score 372.4; DB 4; Length 1864;  
Best Local Similarity 91.2%; Pred. No. 3.le-92;  
Matches 394; Conservative 1; Mismatches 37; Indels 0; Gaps 0;  
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGTGACTTTGTAGGCTAT 60  
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Db 11 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70  
QY 61 AGGCTGAGCAGAAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120  
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Db 71 AAGCTGAGCAGAAAGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCAGCAGCTGAC 130  
QY 121 CCGCTGCACCAAGCCATCGGGGCTGCTGGGAGACGAGTTTGAGACCCCGTTCCGCCGCACC 180  
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Db 131 CCGCTGCACCAAGCCATCGGGGAGCKGGAGATGAGTTCGAGACCCGCTTCGGGCGCACC 190  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACCCAGGTCAGCCCGAGCAACGCTTCACC 240  
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Db 191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGTCAGCCCGAGCAACGCTTCACC 250  
QY 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGCCCTAACTGGGGCCGCTTTGTGGCATTCITT 300  
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Db 251 CAGGTCCTCCGATGAACCTTTTCAAGSGGGCCCCAACTGGGGCCGCTTTGTAGCCTTCITT 310  
QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGGA 360  
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Db 311 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGGAGACACGTCCTGGCTGACTGGATCCACAGC 420  
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Db 371 CAAGTGCAGGAGTGGATGGTGGCCCTACCTGGGAGACGGGCTGGCTGACTGGATCCACAGC 430  
QY 421 AGTGGCGGCTGG 432  
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Db 431 AGTGGGGGCTGG 442  
  
RESULT 6  
US-08-081-448-5  
; Sequence 5, Application US/08081448  
; Patent No. 5646008  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Boise, Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5646008th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,448  
; FILING DATE: 19930622  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. 5646008thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-744-0090  
; TELEFAX: 312-755-4489  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS

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; LOCATION: 135...836
US-08-081-448-5

Query Match      23.1%; Score 134.6; DB 1; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCCGTTCCGCCGACCTTCTCTG 187
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Db 394 AGCAAGCGCTGAGGAGGCGGACGAGTTTGAACCTGCGGTACCGGCGGCATTTCAGTG 453

QY 188 ACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAAGCTTCACCCAGGTTT 247
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Db 454 ACCTGACATCCAGCTCCACATCACCCAGGACAGCATATCAGAGCTTTGAACAGGTAG 513

QY 248 CCGACGAACTTTTCCAAGGGGCCCTAACTGGGCCGCTTGTGGCATTCCTTGTCTCTG 307
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Db 514 TGAATGAACCTCTCCGGGATGGGGTAAACTGGGTGCGCATTTGGCCCTTTTCTCCTCG 573

QY 308 GGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGACAAGTGC 367
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Db 574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGCGGATCG 633

QY 368 AGGATTGGATGGTGGCTACAGCTCTATACGGGGACGGGCCCTGGAGGAGGACGGCGTCTGC 427
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Db 634 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAAGCGCG 693

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Db 694 GCTGGGATACTTTGTGAACTCTATGGGAACAATGCAGCAGCGGAGAGCCGAAAGSGCC 753

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Db 754 AGGAACGCTTCAACCGCTGGTTCTCTGACGGGCATGACTGTGGCGG 798

RESULT 7
US-08-470-670A-6
; Sequence 6, Application US/08470670A
; Patent No. 5834309
; Patent No. 5834309 5710045
; GENERAL INFORMATION:
; APPLICANT: Thompson, Craig B. B.
; APPLICANT: Boise, Lawrence H.
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE:
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,670A
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/081,448
; FILING DATE: 22-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Highlander, Steven L.
; REGISTRATION NUMBER: 37,642
; REFERENCE/DOCKET NUMBER: ARCD:090--1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135...836
US-08-470-670A-6

Query Match      23.1%; Score 134.6; DB 2; Length 926;
Best Local Similarity 58.3%; Pred. No. 1.6e-27;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCCGTTCCGCCGACCTTCTCTG 187
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QY 188 ACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAAGCTTCACCCAGGTTT 247
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Db 454 ACCTGACATCCAGCTCCACATCACCCAGGACAGCATATCAGAGCTTTGAACAGGTAG 513

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Db 574 GCGGGGCACTGTGCGTGGAAAGCGTAGACAAGGAGATGCAGGTATTGGTGCGGATCG 633

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Db 754 AGGAACGCTTCAACCGCTGGTTCTCTGACGGGCATGACTGTGGCGG 798

RESULT 8
US-08-481-739-1
; Sequence 1, Application US/08481739
; Patent No. 6143291
; GENERAL INFORMATION:
; APPLICANT: June, Carl H. and Thompson, Craig B.
; TITLE OF INVENTION: METHODS FOR ENHANCING T CELL SURVIVAL
; TITLE OF INVENTION: BY AUGMENTING BCL-XL PROTEIN LEVELS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,739
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,518
; FILING DATE: 04-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: DeConti, Giulio A. (GAD);
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; REGISTRATION NUMBER: 31,503
; REFERENCE/DOCKET NUMBER: RPI-034CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 926 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 135...836
; US-08-481-739-1

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Query Match	23.1%;	Score 134.6;	DB 3;	Length 926;
Best Local Similarity	58.3%;	Pred. No. 1.6e-27;		
Matches 236;	Conservative 0;	Mismatches 169;	Indels 0;	Gaps 0;

  

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QY	188	ACCTGGCGCTCAGCTACAGTGACCCAGGCTCAGCCCAAGAACGCTTCAACCCAGGTTT	247
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QY	248	CCGACGAACTTTCCAAAGGGGCCCTAACTGGGGCGCTTTCTGGCATCTTTGTCTTTG	307
DB	514	TGAATGAACCTCTCCGGGATGGGTAACTGGGTGCGCATTTGGCCCTTTTCTCCCTCG	573
QY	308	GGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGGGGACAAATGC	367
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QY	368	AGGATTGGATGGTGGCCTACTGGAGACACGCTCTGGCTGACTGGATCCACAGCAGTGGG	427
DB	634	CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCCTGGATCCAGGAGAACGGCG	693
QY	428	GCTGGGGGAGTTTACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGGCTCTGC	487
DB	694	GCTGGGATACTTTTGTGGAACCTATGGGAACAATGCAGCAGCTGAGAGCCGAAAGGCC	753
QY	488	GGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTCTGACGGGGGCGG	532
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QY 368 AGGATTGGATGGTGGCCCTACCTGGAGACAGCTCTGGCTGACTGATCCACAGCAGTGGCG 427  
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Db 754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798

RESULT 11  
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; Sequence 1, Application US/09323743  
; Patent No. 6214986  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, QingQing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0368  
; CURRENT APPLICATION NUMBER: US/09/323,743  
; EARLIER FILING DATE: 1999-06-01  
; EARLIER APPLICATION NUMBER: 09/277,020  
; EARLIER FILING DATE: 1998-03-26  
; EARLIER APPLICATION NUMBER: 09/167,921  
; EARLIER FILING DATE: 1998-10-07  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(836)  
; PUBLICATION INFORMATION:  
; DATABASE ACCESSION NUMBER: L20121 Genbank  
; DATABASE ENTRY DATE: 1994-07-26  
US-09-323-743-1

Query Match 23.1%; Score 134.6; DB 3; Length 926;  
Best Local Similarity 58.3%; Pred. No. 1.6e-27;  
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;  
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Db 394 ASCAAGCGCTGAGGGAGCGCAGCGACGAGTTTGAACTGCGGTACCGGCGGCGCATTCAGTG 453  
QY 188 ACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCAGCAACGCTTACCCAGGTTT 247  
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QY 308 GGGCTGCCCTGTGTGTGAGAGTGTCAACAAGAAATGGAGCCTTTTGGTGGGACAAAGTGC 367  
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QY 368 AGGATTGGATGGTGGCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGCAGTGGCG 427

Db 634 CAGCTTGGATGGCCACTTACCTGAATGATCACCACTAGAGCCTTGGATCCAGGAGAACGGCG 693  
QY 428 GCTGGGGGAGTTACAGCTCTATACGGGGACGGGCCCTGGAGGAGCAGCAGCGCTCTGC 487  
Db 694 GCTGGGATACTTTTGTGGAACCTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 753  
QY 488 GGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTCTGACGGGGGCCG 532  
Db 754 AGGAACGCTTCAACCGCTGGTTCCTGACGGGCATGACTGTGGCCG 798  
RESULT 12  
US-08-461-511A-6  
; Sequence 6, Application US/08461511A  
; Patent No. 6303331  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.B.  
; APPLICANT: Boise, Lawrence H.  
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS  
AND METHODS  
; NUMBER OF SEQUENCES: 18  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/461,511A  
; FILING DATE: 05-Jun-1995  
; CLASSIFICATION: UNKNOWN  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; REFERENCE/DOCKET NUMBER: ARCD:179  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (512) 474-7577  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 135..836  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-461-511A-6

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Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;  
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Db 394 AGCAAGCGCTGAGGGAGCGCAGCGAGTTTGAACTACCGGCGGCGCATTCAGTG 453  
QY 188 ACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCAGCAACGCTTACCCAGGTTT 247  
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; Sequence 5, Application US/09271014A  
; Patent No. 6395510  
; GENERAL INFORMATION:  
; APPLICANT: THOMPSON, CRAIG B.  
; APPLICANT: BOISE, LAWRENCE H.  
; TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS  
; FILE REFERENCE: ARCD:316  
; CURRENT APPLICATION NUMBER: US/09/271,014A  
; NUMBER FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (135)..(836)  
US-09-271-014A-5

Query Match 23.1%; Score 134.6; DB 4; Length 926;  
Best Local Similarity 58.3%; Pred. No. 1.6e-27;  
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;  
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QY 428 GCTGGGCGGAGTTTCACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCACGGCGTCTGC 487  
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; Sequence 6, Application PC/TUS9407089  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: TX  
; COUNTRY: United States of America  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS, ASCII  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07089  
; FILING DATE: CONCURRENTLY FILED  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/081,448  
; FILING DATE: 22 JUNE 1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARKER, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 713-789-2679  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 926 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 135..836  
PCT-US94-07089-6

Query Match 23.1%; Score 134.6; DB 5; Length 926;  
Best Local Similarity 58.3%; Pred. No. 1.6e-27;  
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;  
QY 128 ACCAAGCCATCGGGCTGTGGAGACGAGTTTGAGACCCCGTTTCGGCCGACCTTCTCTG 187  
Db 394 AGCAAGCGCTGAGGGAGCGAGCGGACGAGTTTGAACCTGCGGTACCGGGCGGCAATTCAGTG 453  
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QY 428 GCTGGGCGGAGTTTCACAGCTCTATACGGGGACCGGGCCCTGGAGGAGGCACGGCGTCTGC 487  
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QY 488 GGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTCTGACGGGGGCCG 532



GerCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Scoring table: IDENTITY NJC  
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Searched: 1792395 seqs, 134030451 residues

Total number of hits satisfying chosen parameters: 3584790

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	372.2	64.0	578	12	US-10-029-386-10549
6	371.2	63.8	433	12	US-10-029-386-24249
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8	192.6	33.1	6049	12	US-10-311-455-202
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13	134.6	23.1	702	11	US-09-959-987-9
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18	134.6	23.1	926	14	US-10-072-830-3	Sequence 3, Appli
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c 21	125.8	21.6	555	9	US-09-864-761-24081	Sequence 24081, A
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29	121.8	20.9	6030	14	US-10-171-581-187	Sequence 187, App
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32	117.4	20.2	911	8	US-08-726-211-6	Sequence 6, Appli
33	115.6	19.9	1384	14	US-10-208-155-1	Sequence 1, Appli
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37	63.4	10.9	65	12	US-09-908-975-2435	Sequence 2435, Ap
38	57	9.8	737	10	US-09-952-278-7	Sequence 7, Appli
c 39	56	9.6	6509	12	US-10-311-455-200	Sequence 200, App
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ALIGNMENTS

RESULT 1

US-09-925-674A-8  
; Sequence 8, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 8  
; LENGTH: 582  
; TYPE: DNA  
; ORGANISM: Mouse  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-925-674A-8

Query Match 100.0%; Score 582; DB 10; Length 582;  
Best Local Similarity 100.0%; Pred. No. 2.8e-159;  
Matches 582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
DB	1	ATGGGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
QY	61	AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCCGCGAC 120
DB	61	AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGCCAGCCGCGAC 120
QY	121	CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCGCGACC 180



Db 121 CCGCTGCACCAAGCCATCGGGCTGCTGGAGACGAGTTTGAGACCCCTTTCGGCGGCACC 180  
Qy 181 TTCTCTGACCTGSCGCTCAGCTACACGTGACCCAGGCTCAGCCCAAGAGCTTCACC 240  
Db 181 TTCTCTGACCTGSCGCTCAGCTACACGTGACCCAGGCTCAGCCCAAGAGCTTCACC 240  
Qy 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTCTGTGGCATTCITT 300  
Db 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTCTGTGGCATTCITT 300  
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360  
Db 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360  
Qy 361 CAAGTGCAGGATTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGATTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420  
Qy 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480  
Db 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480  
Qy 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCGTGGCACTG 540  
Qy 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTCTAGCAAGTGA 582  
Db 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTCTAGCAAGTGA 582

RESULT 2  
US-09-925-674A-6  
; Sequence 6, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 583  
; TYPE: DNA  
; ORGANISM: HUMAN  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(579)  
US-09-925-674A-6

Query Match 90.1%; Score 524.4; DB 10; Length 583;  
Best Local Similarity 93.8%; Pred. No. 1.5e-142;  
Matches 546; Conservative 0; Mismatches 36; Indels 0; Gaps 0;  
Qy 1 ATGGCGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 1 ATGGCGACCCAGCCCTCGGCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 60  
Qy 61 AGGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120  
Db 61 AAGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGGCCAGCAGCTGAC 120  
Qy 121 CCGCTGCACCAAGCCATGCGGCTGTCTGTGGAGCAGGTTTGAGACCCGTTTCGGCGGCACC 180  
Db 121 CCGCTGCACCAAGCCATGCGGCGAGCTGGAGATGATGATTCGAGACCCGCTTCGGGCGCACC 180

Qy 181 TTCTCTGACCTGGCGCTCAGCTACACGTGACCCAGGCTCAGCCCAAGAGCTTCACC 240  
Db 181 TTCTCTGATCTGGCGGCTCAGCTGCATGTACCCAGGCTCAGCCCAAGAGCTTCACC 240  
Qy 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGGCCCTAACTGGGGCCGCTCTGTGGCATTCITT 300  
Db 241 CAGGTTTCCGACGAACTTTTCAAGGGGGCCCAACTGGGGCCGCTCTGTAGCCTTCITT 300  
Qy 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360  
Db 301 GTCTTTGGGGCTGCACCTGTGTGCTGAGAGTGTCAACAAGAGATGGAACCACTGGTGGGA 360  
Qy 361 CAAGTGCAGGATTGGATGGTGGCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420  
Db 361 CAAGTGCAGGATGGATGGTGGCTACCTGGAGACCGGCTGGCTGACTGGA:CCACAGC 420  
Qy 421 AGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCACGG 480  
Db 421 AGTGGGGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCAGG 480  
Qy 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCGTGGCACTG 540  
Db 481 CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTCTGACGGGGCCGTGGCACTG 540  
Qy 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTCTAGCAAGTGA 582  
Db 541 GGGGCCCTGGTAACTGTAGGGCCCTTTTCTAGCAAGTGA 582

RESULT 3  
US-09-809-391-130  
; Sequence 130, Application US/09809391  
; Publication No. US20030049618A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruben et al.  
; TITLE OF INVENTION: 186 Human Secreted proteins  
; FILE REFERENCE: P2002P2  
; CURRENT APPLICATION NUMBER: US/09/809,391  
; CURRENT FILING DATE: 2001-03-16  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 761  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 130  
; LENGTH: 1864  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (1648)  
; OTHER INFORMATION: n equals a,t,g, or c  
US-09-809-391-130

Query Match 64.0%; Score 372.4; DB 11; Length 1864;  
Best Local Similarity 91.2%; Pred. No. 2.4e-98;  
Matches 394; Conservative 1; Mismatches 37; Indels 0; Gaps 0;  
Qy 1 ATGGCGACCCAGCCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 11 ATGGCGACCCAGCCCTCGGCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGTTAT 70  
Qy 61 AGGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGAC 120  
Db 71 AAGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCGGGGAGGGCCAGCAGCTGAC 130  
Qy 121 CCGCTGCACCAAGCCATGCGGCTGTCTGTGGAGCAGGTTTGAGACCCGTTTCGGCGGCACC 180  
Db 131 CCGCTGCACCAAGCCATGCGGCGAGCKGGAGATGATTCGAGACCCGCTTCGGGCGCACC 190  
Qy 181 TTCTCTGACCTGGCGGCTCAGCTACACGTGACCCCAAGCTCAGCCCCAGCAACGCTTCACC 240  
Db 191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCAAGCTCAGCCCCAAGCCTTCACC 250



;  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,911  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,599  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,588  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,585  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,586  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,590  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,594  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,593  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,614  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 64.0%; Score 372.4; DB 12; Length 1864;  
Best Local Similarity 91.2%; Pred. No. 2.4e-98;  
Matches 394; Conservative 1; Mismatches 37; Indels 0; Gaps 0;  
  
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGAGGCTAT 60  
|||||  
Db 11 ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 70  
|||||  
  
QY 61 AGGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120  
|||||  
Db 71 AAGCTGAGGCAGAAGGGTTATGTCTGTGGAGCTGGCCCGGGGAGGGCCCGCAGAGTGAC 130  
|||||  
  
QY 121 CCGCTGCACCAAGCCAAGCCATCGGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCGCACC 180  
|||||  
Db 131 CCGCTGCACCAAGCCAAGCCATCGGGGAGCKGGAGATGAGTTCGAGACCCCGCTTCCGGCGCACC 190  
|||||  
  
QY 181 TTCTCTGACCTGGCCGTCAGCTACACGTGACCCAGGCTCAGCCCGAGCAACGCTTCACC 240  
|||||  
Db 191 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCGAGCAACGCTTCACC 250  
|||||  
  
QY 241 CAGTTTCCGACGAACCTTTTCAAGGGGGCCCTAACTGGGGCCGTCTTGTGGCATCTTT 300  
|||||  
Db 251 CAGTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCCGCTTGTAGCCTCTTT 310  
|||||  
  
QY 301 GTCTTTGGGGCTGCCCTGTCTGTCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360  
|||||  
Db 311 GTCTTTGGGGCTGCACCTGTCTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 370  
|||||  
  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAGC 420  
|||||  
Db 371 CAAGTGCAGGAGTGGATGGTGGCCCTACCTGGAGACCGCGGCTGGCTGACTGGATCCACAGC 430  
|||||  
  
QY 421 AGTGGCGGCTGG 432  
|||||  
Db 431 AGTGGCGGCTGG 442  
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RESULT 5  
US-10-029-386-10549  
; Sequence 10549, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO 10549  
; LENGTH: 578  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO CHR14.3  
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3  
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2  
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 0.00e+00  
; OTHER INFORMATION: NT HIT: g114751151, EVALUE 0.00e+00  
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALUE 2.00e-72  
US-10-029-386-10549  
  
Query Match 64.0%; Score 372.2; DB 12; Length 578;  
Best Local Similarity 91.2%; Pred. No. 2.4e-98;  
Matches 395; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

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QY      1  ATGGCGACCCAGCCTCAACCCAGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db      105 ATGGCGACCCAGCCTCGGCCCCAGACACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 164

QY      61  AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGCAC 120
Db      165 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCCGCAGCTGAC 224

QY     121  CCGCTGCACCAAGCCATCGGGCTGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGCAC 180
Db     225 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCGGGCGCAC 284

QY     181  TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Db     285 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 344

QY     241  CAGGTTTCCGACGAACCTTTTCCAAGGGGGCCCTAACTGGGGCCGCTCTTGTGGCATTCCTT 300
Db     345 CAGGTTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCCTT 404

QY     301  GTCTTTGGGCTGCCCTGTCTGTCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360
Db     405 GTCTTTGGGCTGCACGTGTCTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 464

QY     361  CAAAGTCAGGATTGGATGGGCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420
Db     465 CAAAGTCAGGAGTGGATGGTGGCTACCTGGAGACGAGCTGGCTGACTGGATCCACAGC 524

QY     421  ACTGGCGGCTGGG 433
Db     525 ACTGGGGGCTGGG 537

RESULT 6
US-10-029-386-24249
; Sequence 24249, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Arnomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 24249
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 4.2
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALU0.00e+00
; OTHER INFORMATION: SWISSPROT HIT: Q92843, EVALU2.00e-72
; OTHER INFORMATION: NT HIT: gi14751151, EVALU0.00e+00
US-10-029-386-24249
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Query Match      63.8%; Score 371.2; DB 12; Length 433;
Best Local Similarity 91.2%; Pred. No. 4.4e-98;
Matches 394; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY      1  ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db      2  ATGGCGACCCAGCCTCGGCCCCAGACACACGGGCTCTGTGGCAGACTTTGTAGGTTAT 61
```

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QY      61  AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGCAC 120
Db      62  AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCGGGAGGGCCCGCAGCTGAC 121

QY     121  CCGCTGCACCAAGCCATCGGGCTGTCTGTGGAGCTGGAGACGAGTTTGAGACCCGCTTCCGCGCGCAC 180
Db     122 CCGCTGCACCAAGCCATCGGGCAGCTGGAGATGAGTTCGAGACCCGCTTCCGCGCGCAC 181

QY     181  TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCAGGCTCAGCCAGCAACGCTTCACC 240
Db     182 TTCTCTGATCTGGCGGCTCAGTGCATGTGACCCAGGCTCAGCCCAACACGCTTCACC 241

QY     241  CAGGTTTCCGACGAACCTTTTCCAAGGGGGCCCTAACTGGGGCCGCTCTTGTGGCATTCCTT 300
Db     242 CAGGTTCTCCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGCCGCTTGTAGCCTTCCTT 301

QY     301  GTCTTTGGGCTGCCCTGTCTGTCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA 360
Db     302 GTCTTTGGGCTGCACCTGTCTGTCTGAGAGTGTCAACAAGGAGATGGAACCACTGGTGGGA 361

QY     361  CAAAGTCAGGATTGGATGGTGGCTACCTGGAGACACGCTGGCTGACTGGATCCACAGC 420
Db     362 CAAAGTCAGGAGTGGATGGTGGCTACCTGGAGACGAGCTGGCTGACTGGATCCACAGC 421

QY     421  AGTGGCGGCTGG 432
Db     422 AGTGGGGGCTGG 433
```

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RESULT 7
US-10-311-455-201
; Sequence 201, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Det
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 201
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-201
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Query Match      37.6%; Score 218.6; DB 12; Length 6049;
Best Local Similarity 69.1%; Pred. No. 1.3e-53;
Matches 299; Conservative 0; Mismatches 134; Indels 0; Gaps 0;

QY      1  ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
Db     5001 ATGGCGATTTTAGTTTCGGTTTTAGATATACGGGTTTTTGGTGTAGATTTTGTAGGTTAT 5060
```

```
QY      61  AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCGCGCAC 120
Db     5061 AAGTTGAGTAGAAGGGTTATGTTTGTGGAGTTGGTTTCGGGAGGGTTTAGTAGTTGAT 5120

QY     121  CCGCTGCACCAAGCCATCGGGGCTGTCTGTGGAGACGAGTTTGAGACCCGCTTCCGCGCGCAC 180
Db     5121 TCGTTGTATTAGTTATGCGGGTAGTTGGAGATGAGTTCGAGATTCGTTTTCGGCGGTATT 5180
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QY	181	TTCCTGACCTGGCGGTCAAGCTACACGTACCCCAAGGCTCAGCCCAGCAAAGCTTCAAC	240
DG	5181	TTTTTTGATTGGCGGTTTAGTTGTATGTGATTTTAGGTTTAGTTTAATAAAGTTTAT	5240
QY	241	CAGGTTTCCGACGAATTTTCCAAGGGGCCCTAACITGGGSCCGTCTCTTGCGCATCTTT	300
DG	5241	TAGGTTTTCGATGAATTTTAAAGGGGGTTTTTAATTGGGTCTGTTTGTAGTTTTTTT	5300
QY	301	GTCCTTTGGGGCTGCCCTGTGTCTGAGAGTGTCAACAAGAANAATGGAGCCTTTGGTGGGA	360
DG	5301	GTTTITGGGGTGTATTGTGTGTTGAGAGTGTTAATAAGGAGATGGAATTATTGTTGGGA	5360
QY	361	CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACGTCTCTGGCTGACTGGATCCACAGC	420
DG	5361	TAAAGTGTAGGAGTGGATGGTGGTTTATTTCGAGACCGTAGTGGTGGATTGGATTATAGT	5420
QY	421	ASTGGCGGCTGGG	433
DG	5421	ASTGGGGGTGGG	5433

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RESULT 8
US-10-311-455-202/c
; Sequence 202, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determining the Methylation of Cytosine
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; PRIOR FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 202
; LENGTH: 6049
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-202

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	Query Match	33.1%	Score 192.6;	DB 12;	Length 6049;
	Best Local Similarity	66.0%;	Pred. No. 4.9e-46;		
	Matches 279;	Conservative	0;	Mismatches 144;	Indels 0;
QY	1	ATGGCGACCCAGCCTCAACCCGAGACACACGCGGCTCTAGTGGCTGACTTTGTAGGCTAT	63		
Db	1049	ATAACGACCCCAACCTCGACCCCAACACACGGAAGCTCTAATAACAAACTTTATAAAATTAT	990		
QY	61	AGGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGAAAGCCCGCGCGAC	123		
Db	989	AAACTAAACAAAAAATTATATCTATAAAACTAACCCCGAAAAAACCACCAACTAAC	930		
QY	121	CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCGCCGACC	180		
Db	929	CCGCTACACCAAAACCATACGACAACTAAAAATAAATTCGAAACCGGCTTCGACGCAAC	873		
QY	181	TTCTCTGACCTGGCCGCTCAGCTACAGTGACCCCAAGGCTCAGCCCAAGCAACGCTTCACC	240		
Db	869	TTCTTAATCTAACGACTCAACTACATATATAACCCCAAACTCAACCCCAACAAACGCTTCACC	810		
QY	241	CAGGTTTCCGACGAACTTTTTCCAAGGGGGCCCTAACTGGGGCCGCTCTTTGTGGCATTCCTTT	300		
Db	809	CAAACTCTCCGATAAACTTTTCAAAAAAACCACCACTAAACAGGCTTATAAACCTTCCTTT	750		

[illegible]

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RESULT 9
US-10-029-386-27084
; Sequence 27084, Application US/10029386
; Publication NO. US20030194704A
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: AEOMICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 27084
; LENGTH: 151
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 5.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
; OTHER INFORMATION: NT HIT: gi14574571, EVALUE 9.00e-80
US-10-029-386-27084

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Query Match 25.7%; Score 149.4; DB 12; Length 151;  
Best Local Similarity 99.3%; Pred. No. 9.8e-34;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	432	GGCGAGTTACAGCTCTATACGGGACGGGCCCTGGAGGAGGCACGGCGTCTGCGGGA	491
Db	1	GGCGAGTTACAGCTCTATACGGGACGGGCCCTGGAGGAGGCAGCGCGTCTGCGGGA	60
Qy	492	GGGAACTGGGCATCAGTGAAGGACAGTGTGACGGGGGCGCTGGCACTGGGGGCGCTGGT	551
Db	61	GGGAACTGGGCATCAGTGAAGGACAGTGTGACGGGGGCGCTGGCACTGGGGGCGCTGGT	120
Qy	552	AACTGTAGGGGCGCTTTTTCCTAGCAAGTGA	582
Db	121	AACTGTAGGGGCGCTTTTTCCTAGCAAGTGA	151

RESULT 10  
US-10-029-386-13384  
; Sequence 13384, Application US/10029386  
; Publication No. US20030194704A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharron G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO  
; FILE REFERENCE: AEOMICA-X-2  
; CURRENT APPLICATION NUMBER: US/10/029,386  
; CURRENT FILING DATE: 2001-12-20  
; NUMBER OF SEQ ID NOS: 34288

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; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13384
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.2
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 2.00e-10
; OTHER INFORMATION: NT HIT: g14751151, EVALUE 0.00e+00
; OTHER INFORMATION: EST_HUMAN HIT: AL157542.1, EVALUE 1.00e-119
US-10-029-386-13384
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Query Match          25.7%; Score 149.4; DB 12; Length 590;
Best Local Similarity 99.3%; Pred. No. 1.2e-33;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 432 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGGCGTCTGCGGGA 492
      |||||||
Db 25 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGGCGTCTGCGGGA 84
      |||||||

QY 492 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGT 552
      |||||||
Db 85 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGT 144

QY 552 AACTGTAGGGGCCTTTTGTGCTAGCAAGTGA 582
      |||||||
Db 145 AACTGTAGGGGCCTTTTGTGCTAGCAAGTGA 175
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RESULT 11
US-09-864-761-17690
; Sequence 17690, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
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; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 17690
; LENGTH: 150
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO ALC49829.2
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 2.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.94
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
; OTHER INFORMATION: NT HIT: D87461.1, EVALUE 2.00e-79
; OTHER INFORMATION: EST HUMAN HIT: AL157542.1, EVALUE 8.00e-70
; OTHER INFORMATION: SWISSPROT HIT: P70345, EVALUE 3.00e-11
US-09-864-761-17690

Query Match          25.5%; Score 148.4; DB 9; Length 150;
Best Local Similarity 99.3%; Pred. No. 1.9e-33;
Matches 149; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 433 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAG 492
      |||||||
Db 1 GCGGAGTTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGGCGTCTGCGGGAG 60

QY 493 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGTA 552
      |||||||
Db 61 GGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCCGTGGCACTGGGGCCCTGGTA 120

QY 553 ACTGTAGGGGCCTTTTGTGCTAGCAAGTGA 582
      |||||||
Db 121 ACTGTAGGGGCCTTTTGTGCTAGCAAGTGA 150
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RESULT 12
US-10-169-223-13
; Sequence 13, Application US/10169223
; Publication No. US20030152946A1
; GENERAL INFORMATION:
; APPLICANT: SHIMIZU, Shigeomi
; APPLICANT: TSUJIMOTO, Yoshihide
; TITLE OF INVENTION: BH4-Fused Polypeptides
; FILE REFERENCE: 1422-0537p
; CURRENT APPLICATION NUMBER: US/10/169,223
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: JP 11-371449
; PRIOR FILING DATE: 1999-12-27
; PRIOR APPLICATION NUMBER: PCT/JP00/09274
; PRIOR FILING DATE: 2000-12-26
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 636
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized DNA for mutant bcl-xL
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (1)..(636)
; OTHER INFORMATION:
US-10-169-223-13
Query Match      23.1%; Score 134.6; DB 12; Length 636;
Best Local Similarity 58.3%; Pred. No. 2.4e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCGCGCACCTTCTCTG 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 197 AGCAAGCGCTGAGGAGGCGAGCGACGAGTTTGAACCTGCGGTACCGCGCGGCATTTCAGTG 256
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 188 ACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGAGCAACGCTTCACCCAGGTTT 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 257 ACCTGACATCCCAGCTCCACATCACCCCGAGGACAGCATATCAGAGCTTTGAACAGGTAG 316
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCCGCTCTTGTGSGCATTTCTTTGTCCTTG 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 317 TGAATGAACCTTTCGGGATGGGGTAAACTGGGGTCGCATTGTGSGCCTTTTCTCCTTCG 376
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 GGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGACAAAGTGC 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 377 GCGGGGCACGTGCGGTGGAAGCGTAGACAAGAGATGCAGGTATTGTTGAGTCGGATCG 436
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 AGGATTGGATGGTGGCCCTACCTGGAGACACGTCTGTGCTGACTGGATCCACAGCAGTGGCG 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 437 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 496
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 GCTGGCGGAGTTTCACAGCTCTATACGGGGAGCGGGCCCTGGAGGAGGACGGCGTCTGC 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 497 GCTGGGATACTTTTGTGGAACCTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 556
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 GGGAGGGGAACCTGGGCATCAGTGAGGACAGTGCTGACGGGGGGCGG 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 557 AGGAACGCTTCAACCGCTGGTTCTCTGACGGGCATGACTGTGGCGG 601
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RESULT 13

```

US-09-959-987-9
; Sequence 9, Application US/09959987
; Publication No. US200300400i2A1
; GENERAL INFORMATION:
; APPLICANT: Japan Science and Technology Corporation
; TITLE OF INVENTION: A Detection Method of Protein-Protein Interaction
; FILE REFERENCE: 2001_1695A/WMC/00653
; CURRENT APPLICATION NUMBER: US/09/959,987
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/JP01/01973
; PRIOR FILING DATE: 2001-03-13
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 702
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(702)
US-09-959-987-9
Query Match      23.1%; Score 134.6; DB 11; Length 702;
Best Local Similarity 58.3%; Pred. No. 2.4e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCGCGCACCTTCTCTG 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 260 AGCAAGCGCTGAGGAGGCGAGCGGACGAGTTTGAACCTGCGGTACCGGCGGCGCATTCAGTG 319
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 188 ACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGAGCAACGCTTCACCCAGGTTT 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 320 ACCTGACATCCCAGCTCCACATCACCCCGAGGACAGCATATCAGAGCTTTGAACAGGTAG 379
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCGGCTCTTGTGGCATTTCTTGTCTTG 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 380 TGAATGAACCTTTCGGGATGGGTAAACTGGGTGCGCATTTGTGGCCTTTTCTCCTTCG 439
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 GGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGACAAAGTGC 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 440 GCGGGGCACGTGCTGCTGGAAGCGTAGACAAGGAGATGCAGGTATTGTTGAGTCGGATCG 499
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 368 AGGATTGGATGGTGGCCCTACCTGGAGACACGTCTGTGCTGACTGGATCCACAGCAGTGGCG 427
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 500 CAGCTTGGATGGCCACTTACCTGAATGACCACCTAGAGCCTTGGATCCAGGAGAACGGCG 559
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 428 GCTGGCGGAGTTTCACAGCTCTATACGGGGAGCGGGCCCTGGAGGAGGACGGCGTCTGC 487
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 560 GCTGGGATACTTTTGTGGAACCTCTATGGGAACAATGCAGCAGCCGAGAGCCGAAAGGGCC 619
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 488 GGGAGGGGAACCTGGGCATCAGTGAGGACAGTCTGACGGGGGGCGG 532
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 620 AGGAACGCTTCAACCCGCTGGTTCTCTGACGGGCATGACTGTGGCGG 664
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
US-09-734-846-1
; Sequence 1, Application US/09734846
; Patent No. US20010007025A1
; GENERAL INFORMATION:
; APPLICANT: Bennett, C. Frank
; APPLICANT: Dean, Nicholas M.
; APPLICANT: Monia, Brett P.
; APPLICANT: Nickoloff, Brian J.
; APPLICANT: Zhang, QingQing
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression
; FILE REFERENCE: ISPH-0528
; CURRENT APPLICATION NUMBER: US/09/734,846
; CURRENT FILING DATE: 2000-12-12
; PRIOR APPLICATION NUMBER: 09/277,020
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 09/167,921
; PRIOR FILING DATE: 1998-10-07
; PRIOR APPLICATION NUMBER: 09/323,743
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 926
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (135)..(836)
; DATABASE ACCESSION NUMBER: L20121 Genbank
; DATABASE ENTRY DATE: 1994-07-26
US-09-734-846-1
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Query Match      23.1%; Score 134.6; DB 9; Length 926;
Best Local Similarity 58.3%; Pred. No. 2.5e-29;
Matches 236; Conservative 0; Mismatches 169; Indels 0; Gaps 0;

QY 128 ACCAAGCCATGCGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGCGCGCACCTTCTCTG 187
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 394 AGCAAGCGCTGAGGAGGCGAGCGGACGAGTTTGAACCTGCGGTACCGGCGGCGCATTCAGTG 453
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 188 ACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGAGCAACGCTTCACCCAGGTTT 247
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 454 ACCTGACATCCAGCTCCACATCACCCCGAGGACAGCATATCAGAGCTTTTGAACAGGTAG 513
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 248 CCGACGAACTTTTCCAAGGGGGCCCTAACTGGGGCGGCTTGTGGCATTTCTTTGTCTTG 307
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 514 TGAATGAACCTTTCGGGATGGGGTAAACTGGGGTCCGATTTGTGGCCTTTTCTCCTTCG 573
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 308 GGGCTGCCCTGTGCTGAGAGTGTCAACAAGAAATGAGAGCCTTTGGTGGGACAAAGTGC 367
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 574 GCGGGCACCTGTGCGTGGAAAGCGTAGACAAGAGATGCAGGTATTGTTGAGTGGATCG 633
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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GenCore version 5.1.6  
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OMnucleic - nucleic search, using sw model

Run on: October 27, 2003, 11:50:55 ; Search time 1467.74 Seconds  
(without alignments)  
9637.411 Million cell updates/sec

Title: US-09-925-674A-8  
Perfect score: 582  
Sequence: 1 atggcgacccagctctaac.....ccttttttgcctagcaagtga 582

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*  
28: gb\_gss1:\*  
29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	578.8	99.5	1949	11 AK015644	AK015644 Mus muscu
2	578.8	99.5	3487	11 AK004680	AK004680 Mus muscu
3	577.2	99.2	969	14 BY715200	BY715200 BY715200
4	521.2	89.6	967	13 BU503850	BU503850 AGENCOURT

5	496.2	85.3	804	9	AL157542
6	495.6	85.2	1030	10	BE793530
7	445	76.5	815	10	BF785386
8	430.6	74.0	697	12	BI770566
9	429.8	73.8	854	11	AK013244
10	417	71.6	792	10	BG298789
11	415.4	71.4	623	14	CB578463
12	411.6	70.7	540	9	AW258810
13	391.8	67.3	626	14	CA391923
14	366.8	63.0	643	12	BI910270
15	358.4	61.6	440	14	CB749817
16	353.2	60.7	559	14	BY704881
17	351.2	60.3	437	14	CB790932
18	335.6	57.7	869	13	BU557268
19	335.6	57.7	872	13	BU557410
20	330.2	56.7	548	14	CA407899
21	328.6	56.5	645	14	BY740551
22	325.4	55.9	362	9	AA596919
23	313.2	53.8	410	14	CB804140
24	308	52.9	460	13	BY285647
25	302.8	52.0	449	13	BY253191
26	294.4	50.6	1053	13	BU931540
27	286.8	49.3	758	12	BI764428
28	277.4	47.7	457	10	BB856021
29	273.4	47.0	430	14	CB760687
30	270	46.4	425	13	BY251598
31	267	45.9	467	13	BY253189
32	264.8	45.5	302	13	BY356166
33	262.2	45.1	305	13	BY356183
34	254.2	43.7	749	10	BG677345
35	253.4	43.5	353	13	BY312773
36	246.8	42.4	601	10	BF204905
37	246.4	42.3	375	13	BY302913
38	245.8	42.2	1064	13	BQ646339
39	244.4	42.0	372	13	BY133304
40	243.6	41.9	452	14	CB786193
41	243.2	41.8	314	13	BY356000
42	241.2	41.4	853	14	CA984774
43	235.8	40.5	365	13	BY136977
44	233.6	40.1	433	9	AW326901
45	227.8	39.1	358	13	BY302899

ALIGNMENTS

RESULT :  
AK015644  
LOCUS  
DEFINITION  
AK015644 1949 bp mRNA linear HTC 05-DEC-2002  
Mus musculus adult male testis cDNA, RIKEN full-length enriched  
library, clone:4930488D08 product:Bcl2-like 2, full insert  
sequence.  
ACCESSION  
AK015644  
VERSION  
AK015644.1 GI:12854052  
KEYWORDS  
HTC; CAP trapper.  
SOURCE  
Mus musculus (house mouse)  
ORGANISM  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
REFERENCE  
1  
Carninci,P. and Hayashizaki,Y.  
AUTHORS  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
TITLE  
High-efficiency full-length cDNA cloning  
JOURNAL  
Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE  
99279253  
PUBMED  
10349636  
REFERENCE  
2  
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,  
AUTHORS  
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE  
Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL  
Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE  
20499374  
PUBMED  
11042159



Db	612	CGTCTGGGGAGGGGAAGTGGGCATCGTAGGACAGTCTGACGGGCGGTGGCAC	671
QY	541	GGGGCCCTGGTAAC	582
Db	672	GGGGCCCTGGTAAC	713
RESULT 2			
AK004680			
LOCUS			
DEFINITION	AK004680	3487 bp	linear mRNA
ACCESSION	AK004680		
VERSION	AK004680.1	GI:12836027	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Carninci,P. and Hayashizaki,Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999);		
MEDLINE	99279253		
PUBMED	10349636		
REFERENCE	2 Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.		
AUTHORS	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
TITLE	Genome Res. 10 (10), 1617-1630 (2000)		
JOURNAL	20499374		
MEDLINE	11042159		
PUBMED	3		
REFERENCE	Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsuai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,C., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.		
AUTHORS	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
TITLE	Genome Res. 10 (11), 1757-1771 (2000)		
JOURNAL	20530913		
MEDLINE	11076861		
PUBMED	4		
REFERENCE	Kawai,J., Shiragawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y., Arakawa,T., Hara,A., Fukunishi,Y., Konno,H., Adachi,S., Fukuda,S., Aizawa,K., Izawa,M., Nishi,K., Kiyosawa,H., Kondo,S., Yamaraka,I., Saito,T., Okazaki,Y., Gojcbori,T., Bono,H., Kasukawa,T., Saito,R., Kadota,K., Matsuda,H., Ashburner,M., Batalov,S., Casavant,T., Fleischmann,W., Gaasterland,T., Gissi,C., King,B., Kochiwa,H., Kuehl,P., Lewis,S., Matsuo,Y., Nikaio,I., Pesole,G., Tomita,M., Quackenbush,J., Schriml,L.M., Staubli,F., Suzuki,R., Mitsui,M., Wagner,L., Washio,T., Sakai,K., Okido,T., Furuno,M., Aono,H., Baldarelli,R., Barsh,G., Blake,J., Boffelli,D., Bojunga,N., Carninci,P., de Bonaldo,M.F., Brownstein,M.J., Bult,C., Fletcher,C., Fujita,M., Gariboldi,M., Gustincich,S., Hill,D., Hofmann,M., Hume,D.A., Kamiya,M., Lee,N.H., Lyons,P., Marchionni,L., Mashima,J., Mazzarelli,J., Mombaerts,P., Nordone,P., Ring,B., Ringwald,M., Rodriguez,I., Sakamoto,N., Sasaki,H., Sato,K., Schonbach,C., Seya,T., Shibata,Y., Storch,K.F., Suzuki,H., Toyo-oka,K., Wang,K.H., Weitz,C., Wittaker,C., Wilming,L., Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohtsuki,S. and Hayashizaki,Y.		
AUTHORS	Functional annotation of a full-length mouse cDNA collection		
TITLE	Nature 409 (6821), 685-690 (2001)		
JOURNAL	21085660		
MEDLINE	11217851		
PUBMED	5		
REFERENCE	The FANTOM Consortium and the RIKEN Genome Exploration Research		
AUTHORS			

TITLE	Group Phase I & II Team.
JOURNAL	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
REFERENCE	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 3487)
	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE	Direct Submission
JOURNAL	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT	Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGCGCGCAACTCGAGTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence[5' GAGAGAGAGGATCCAGAGCTCAATTATTTAATTAACCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: SstI; 3' end: XhoI. Host: SOLR.
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	/db_xref="MGI:1896837"
	/db_xref="taxon:10090"
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	/sex="male"
	/tissue_type="lung"
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	/dev_stage="adult"
	209..790
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	/db_xref="MGI:108052"
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	3466..3471
	/note="putative"
	3487
	/note="putative"
	BASE COUNT 777 a 834 c 990 g 886 t
ORIGIN	
	Query Match 99.5%; Score 578.8; DB 1; Length 3487;
	Best Local Similarity 99.7%; Pred. No. 2.8e-135;

Matches	580;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
QY	1	ATGGCGACCCCGCCTCAACCCCGACACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT	60						
DB	209	ATGGCGACCCCGCCTCAACCCCGACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT	268						
QY	61	AGGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGCGCCCTGGGGAAGCCAGCCGCCGAC	120						
DB	269	AAGCTGAGGCAGAAAGGTTATGTCTGTGGAGCTGCGCCCTGGGGAAGCCAGCCGCCGAC	328						
QY	121	CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCCGTTCCGCCGCACC	180						
DB	329	CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCCGTTCCGCCGCACC	388						
QY	181	TTCTCTGACCTGGCGCTCAGCTACACGTGACCCGAGGCTCAGCCGACGCTTTCACC	240						
DB	389	TTCTCTGACCTGGCGCTCAGCTACACGTGACCCGAGGCTCAGCCGACGACGCTTTCACC	448						
QY	241	CAGGTTTCCGACGAACTTTCCAAAGGGGGCCCTAACTGGGGCCGCTCTTGTGGCATTCTT	300						
DB	449	CAGGTTTCCGACGAACTTTCCAAAGGGGGCCCTAACTGGGGCCGCTCTTGTGGCATTCTT	508						
QY	301	GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA	360						
DB	509	GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCTTTGGTGGGA	569						
QY	361	CAAGTGCAGGATTGGTGGCCTACCTGGACACACGTCTGGCTGACTGGATCCACAGC	420						
DB	569	CAAGTGCAGGATTGGTGGCCTACCTGGACACACGTCTGGCTGACTGGATCCACAGC	628						
QY	421	AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGG	480						
DB	629	AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGCACGG	688						
QY	481	CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCGGTGGCACTG	540						
DB	689	CGTCTGCGGGAGGGAACTGGGCATCAGTGAGGACAGTGCTGACGGGGCGGTGGCACTG	748						
QY	541	GGGGCCCTGGTAACTGTAGGGGCCCTTTTTCCTAGCAAGTGA	582						
DB	749	GGGGCCCTGGTAACTGTAGGGGCCCTTTTTCCTAGCAAGTGA	790						
RESULT 3									
BY715200									
LOCUS									
DEFINITION	BY715200	RIKEN full-length enriched, adult male testis	Mus musculus						
ACCESSION	BY715200								
VERSION	EST.								
KEYWORDS	Mus musculus (house mouse)								
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS									

	R.D., Tomita,M., Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watanabe,Y., Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I., Yang,L., Yuan,Z., Zavolar,M., Zhu,Y., Zimmer,A., Carninci,P., Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,C., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,Y., Takeda,Y., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
TITLE	Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
JOURNAL	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
PUBMED	Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken prepared mouse tissues. Please visit our web site ( <a href="http://genome.gsc.riken.go.jp">http://genome.gsc.riken.go.jp</a> ) for further details.
FEATURES	Location/Qualifiers
source	1. .969
	/organism="Mus musculus"
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	/strain="C57BL/6J"
	/db_xref="taxon:10090"
	/clone="4930488D08"
	/sex="male"
	/tissue_type="testis"
	/dev_stage="adult"
	/lab_host="SOLR"
	/clone_lib="RIKEN full-length enriched, adult male testis"
	/note="Site 1: XhoI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5' GAGAGAGAAGGATCCAGAGCTCTTTTCTTTTCTTTT 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'



GAGAGAGAGAGCGCGGCAATTAATTCGAGTTAATTAATAATCCCGCCCCCCC  
3'). cDNA was cloned into the XhoI and BamHI sites. "

BASE COUNT 195 a 242 c 345 g 181 t 6 others  
ORIGIN

Query Match 99.2%; Score 577.2; DB 14; Length 969;  
Best Local Similarity 99.5%; Pred. No. 5e-135;  
Matches 579; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGGCGACCCAGCCTCAACCCCGACACACCGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
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Db 132 ATGGCGACCCAGCCTCAACCCCGACACACCGGGCTCTAGTGGCTGACTTTGTAGGCTAT 191  
|||  
QY 61 AGGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCGGAC 120  
|||  
Db 192 AAGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCGGAC 251  
|||  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCCGCACC 180  
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Db 252 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCCGTTTCCGCCCGCACC 311  
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QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGACCAACGCTTCACC 240  
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Db 312 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGACCAACGCTTCACC 371  
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QY 241 CAGGTTTCCGACGAACCTTTTCCAGGGGGCCCTAACTGGGGCGGTCTTGTGGCATTCCTT 300  
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QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGTGGGA 360  
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Db 432 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGTGGGA 491  
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QY 361 CAAGTCAGGATTGGAATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 420  
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Db 492 CAAGTCAGGATTGGAATGGTGGCCCTACCTGGAGACACAGTCTGGCTGACTGGATCCACAGC 551  
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QY 421 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGACAGG 480  
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Db 552 AGTGGCGGCTGGCGGAGTTCACAGCTCTATACGGGACGGGGCCCTGGAGGAGGACAGG 611  
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QY 481 CGTCTGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTACGGGGCGGCGCTGGCACTG 540  
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Db 612 CGTCTGGGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTACGGGGCGGCGCTGGCACTG 671  
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QY 541 GGGGCCCTGGTAACCTGTAGGGCCCTTTTGTCTAGCAAGTGA 582  
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Db 672 GGGGCTCTGGTAACCTGTAGGGCCCTTTTGTCTAGCAAGTGA 713  
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RESULT 4  
BU503850 967 bp mRNA linear EST 12-SEP-2002  
LOCUS AGENCOURT\_10030867 NIH\_MGC\_94 Mus musculus cDNA clone IMAGE:6491566  
DEFINITION 5', mRNA sequence.  
ACCESSION BU503850  
VERSION BU503850.1 GI:22810083  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 967)

NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: The Cepko Laboratory  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM14043 row: c column: 23  
High quality sequence stop: 524.  
FEATURES  
Location/Qualifiers  
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Average insert size 3.3 kb. Library enriched for  
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Note: this is a NIH\_MGC Library."  
BASE COUNT 199 a 255 c 348 g 165 t  
ORIGIN

Query Match 89.6%; Score 521.2; DB 13; Length 967;  
Best Local Similarity 98.6%; Pred. No. 6.7e-121;  
Matches 578; Conservative 0; Mismatches 3; Indels 5; Gaps 5;

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QY 61 AGGCTGAGGCAGAAGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCGGAC 120  
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QY 121 CCGCTGCACCAAGCCATGCGGGCTGTGGAGACGAGTTTGAGACCCGTTTCCGCCCGCACC 180  
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QY 181 TTCTCTGACCTGGCCGCTCAGCTACAGTACACCGGCTCAGCCCGAGGCTCAGCCAGCAACGCTTCACC 240  
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QY 361 CAAGTCAGGATTGGATGGTGGCCTA-CCTGGAGACACGCTCTGGCTGACTGGATCCACAG 419  
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Db 490 CAAGTCAGGATTGGATGGTGGCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAG 549  
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QY 420 CAGT-GGCGGTGGCGGAGTTCACAGCTCTATACGGGAC-GGGGCCCTGGAGGAGCA 477  
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Db 550 CAGTGGGGGCTGGCGGAGTTCACAGCTTATACGGGACGGGGCCCTGGAGGAGCA 609  
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QY 478 CGGCGTCTGGCGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGTGAC-GGGGGCCGTGGC 536  
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Db 610 CGGCGTCTGGCGGAGGGGAACCTGGGCATCAGTGAGGACAGTGTGTGACGGGGGGCCGTGGC 669  
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QY 537 ACTGGGGGCCCTGGTAACCTGT-AGGGGCCCTTTTGTCTAGCAAGTG 581  
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Db 670 ACTGGGGGCCCTGGTACCTGTAAAGGGGCCCTTTTGTCTAGCAAGTG 715  
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RESULT 5  
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LOCUS DKFZp761D0816.r1 761 (synonym: hamy2) Homo sapiens cDNA clone  
DEFINITION DKFZp761D0816\_5', mRNA sequence.  
ACCESSION AL157542  
VERSION AL157542.1 GI:7057943

KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
AUTHORS i (bases 1 to 804)  
TITLE Ansoerge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.  
JOURNAL EST (Ansoerge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)  
COMMENT Unpublished  
Contact: Ansoerge W  
MIPS  
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@kfz-heidelberg.de;  
sequenced by EMBL (European Molecular Biology Laboratories,  
Heidelberg/Germany) within the cDNA sequencing consortium of the  
German Genome Project.  
No sl sequence available.  
This clone (DKFZp761D0816) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
FEATURES  
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Best Local Similarity 93.0%; Pred. No. 1.3e-114;  
Matches 541; Conservative 0; Mismatches 39; Indels 2; Gaps 2;  
QY 1 ATGGCGACCCAGCCCTCAACCCCCAGACACACCGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
DB 134 ATGGCGACCCAGCCCTCGGCCCCAGACACACCGGCTCTGTGGCAGACTTTGTAGGTTAT 193  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCAGCCCGGAC 120  
DB 194 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCCGGGAGGGCCAGCAGCTGAC 253  
QY 121 CCGCTGCACCAAGCCATCGGGGCTGTCTGGAGCAGATTGTGAGACCCGTTCCGCCGCACC 180  
DB 254 CCGCTGCACCAAGCCATCGGGGAGCTGGAGATGAGTTCGAGACCCCGTTCCGGCGCACC 313  
QY 191 TTCTCTGACCTGGCGCTCAGCTACAGTACACGTCACCCAGGCTCAGCCCAAGCAGCTTCACC 240  
DB 314 TTCTCTGATCTGGCGCTCAGCTGCATGTGACCCCAAGGCTCAGCCCAAGCAGCTTCACC 373  
QY 241 CAGGTTTCCGACGAACTTTTCCAAGGGGCCCTAACTGGGGCCGCTCTGTGGCATTCTTT 300  
DB 374 CAGGTCTCCGATGAAGTTTTC AAGGGGCCCAACTGGGGCCGCTGTAGCCTTCTTT 433  
QY 301 GTCTTTGGGGCTGCCCTGTGTCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360  
DB 434 GTCTTTGGGGCTGCACCTGTGTGCGNAGAGTGTCAACAAAGGAGATGGAACCACTGGTGGGA 493  
QY 361 CAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACAGTCTGTGGCTGACTGGATCCACAGC 420  
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AUTHORS i (bases 1 to 1030)  
TITLE NIH-MGC http://mgc.nci.nih.gov/.  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: DCTD/DTP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov  
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TITLE  
JOURNAL  
COMMENT

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1 (bases 1 to 815)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
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AUTHORS  
TITLE  
JOURNAL  
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1 (bases 1 to 697)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
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Location/Qualifiers

FEATURES



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primed, and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.4 kb, insert size
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this is a NIH_MGC Library."
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VERSION AK013244.1 GI:12850487
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Mus musculus (house mouse)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
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2
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
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3
Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
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RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
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4
Kawai,J., Shinagawa,A., Shibata,K., Yoshino,M., Itoh,M., Ishii,Y.,
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Wynshaw-Boris,A., Yoshida,K., Hasegawa,Y., Kawaji,H., Kohsaki,S.
and Hayashizaki,Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
21085660
11217851
5
The PANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 854)
Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
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Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T.,
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Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,  
Yoshino,M., Muramatsu,M. and Hayashizaki,Y.  
Direct Submission  
Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)  
Please visit our web site (http://genome.gsc.riken.go.jp/) for  
further details.  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues. First strand cDNA was primed with a primer  
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and subsequently enriched for full-length by cap-trapper. cDNA went  
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1 (bases 1 to 792)  
NIH-MGC http://mgc.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: The Cepko Laboratory  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
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/db\_xref="taxon:10090"  
/clone="IMAGE:4511215"  
/tissue\_type="retina"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH\_MGC\_94"  
/note="Organ: eye; Vector: pCMV-SPORT6; Site\_1: NotI;  
Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.  
Average insert size 3.3 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH MGC Library."  
BASE COUNT 174 a 201 c 246 g 171 t  
ORIGIN

Query Match 71.6%; Score 417; DB 10; Length 792;  
Best Local Similarity 98.6%; Pred. No. 1.2e-94;  
Matches 431; Conservative 0; Mismatches 5; Indels 1; Gaps 1;  
QY 1 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db 99 ATGGCGACCCAGCCTCAACCCAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 158  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGCCCGCCGAC 120  
Db 159 AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGCCCGCCGAC 218

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QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGGCGGCACC 180
    |||
Db 219 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGGCGGCACC 278

QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGTCAGCCCGAGCAACGCTTCACC 240
    |||
Db 279 TTCTCTGACCTGG-CGCTCAGCTACACGTGACCCCGAGGTCAGCCCGAGCAACGCTTCACC 337

QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCTAACTGGGCCCGTCTTGTGGCATTCCTT 300
    |||
Db 338 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCTAACTGGGCCCGTCTTGTGGCATTCCTT 397

QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360
    |||
Db 398 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 457

QY 361 CAAGTGCAGGATTGGATGGTGGGCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC 420
    |||
Db 458 CAAGTGCAGGATTGGATGGTGGGCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC 517

QY 421 AGTGGCGGCTGGSCGGA 437
    |||
Db 518 AGTGGCGGCTGGTAAGA 534

RESULT 11
LOCUS CB578463
DEFINITION CB578463 623 bp mRNA linear EST 03-APR-2003
clone nrdg1-00100-h10-A nrdg1 (10855) Rattus norvegicus cDNA
ACCESSION CB578463
VERSION CB578463.1 GI:29522504
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
REFERENCE 1 (bases 1 to 623)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00100 row: h column: 10.
Location/Qualifiers
1. .623
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="nrdg1-00100-h10"
/tissue_type="Dorsal Root Ganglia"
/clone_lib="nrdg1 (10855)"
/note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; rat dorsal root ganglia"
BASE COUNT 114 a 207 c 184 g 118 t
ORIGIN

Query Match 71.4%; Score 415.4; DB 14; Length 623;
Best Local Similarity 97.5%; Pred. No. 2.9e-94;
Matches 422; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 ATGGGACCCCGAGCCTCAACCCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60
    |||
Db 191 ATGGGACCCCGAGCCTCAACCCCGAGACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 250

QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120
    |||
Db 251 AAGCTGAGGCAGAGGGTTATGTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 310

QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCGGCGGCACC 180
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Db 311 CCGCTGCACCAAGCCATGCGGGGAGCTGGAGACGAGTTTGAGACCCGCTTCGGCGGCACC 370
    |||
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGTCAGCCCGAGCAACGCTTCACC 240
    |||
Db 371 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGTCAGCCCGAGCAACGCTTCACC 430

QY 241 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCTAACTGGGCCCGTCTTGTGGCATTCCTT 300
    |||
Db 431 CAGGTTTCCGACGAACTTTTCCAAAGGGGCCCTAACTGGGCCCGTCTTGTGGCATTCCTT 490

QY 301 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCCTTTGGTGGGA 360
    |||
Db 491 GTCTTTGGGGCTGCCCTGTGTGCTGAGAGTGTCAACAAGAAATGGAGCCATTTGGTGGGA 550

QY 361 CAAGTGCAGGATTGGATGGTGGGCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC 420
    |||
Db 551 CAAGTGCAGGATTGGATGGTGGGCTACCTGGAGACACGTCGTGGCTGACTGGATCCACAGC 610

QY 421 AGTGGCGGCTGGG 433
    |||
Db 611 AGTGGCGGCTGGG 623

RESULT 12
LOCUS AW258810
DEFINITION AW258810 540 bp mRNA linear EST 23-DEC-1999
um74a02.y1 Sugano mouse kidney mkia Mus musculus cDNA clone
IMAGE:2300906 5' similar to SW:BCLW_MOUSE P70345 APOPTOSIS
REGULATOR BCL-W. [2] SW:BCLW_MOUSE ;, mRNA sequence.
ACCESSION AW258810
VERSION AW258810.1 GI:6631791
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 540)
AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,C., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE The WashU-NCI Mouse EST Project 1999
JOURNAL Unpublished
COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:1009678
Seq primer: custom primer used
High quality sequence stop: 465.
Location/Qualifiers
1. .540
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:2300906"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse kidney mkia"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII (CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCCTACTGG], digested and cloned into distinct DraIII sites of the pME18S-FL3
```

vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAAGCTGG and 3' end primer CGACCTGCAGCTGAGCACA."

BASE COUNT 98 a 165 c 170 g 107 t  
ORIGIN

Query Match 70.7%; Score 411.6; DB 9; Length 540;  
Best Local Similarity 98.8%; Pred. No. 2.5e-93;  
Matches 425; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

QY 1 ATGGCGACCCCGAGCTCAACCCACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
112 ATGGCGACCCCGAGCTCAACCCACACACACGGGCTCTAGTGGCTGACTTTGTAGGCTAT 171  
QY 61 AGGCTGAGGCAGAGGGTTATGCTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
172 AAGCTGAGGCAGAGGGTTATGCTCTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 231  
QY 121 CCGCTGACCAAGCCATGCGGGCTGTGTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
232 CCGCTGACCAAGCCATGCGGGCTGTGTGTGGAGCTGGCCCTGGGGAAGGCCCGCCGAC 291  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGCTGACCCCGAGCAAGCTTCACC 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
292 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGCTGACCCCGAGCAAGCTTCACC 351  
QY 241 CAGGTTCCGACGAACCTTTTCCAAAGGGGGCCCTAACTGGGGCGCTCTTGTGGCATTTT 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
352 CAGGTTCCGACGAACCTTTTCCAAAGGGGGCCCTAACTGGGGCGCTCTTGTGGCATTTT 411  
QY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
412 GTCTATGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGA 471  
QY 361 CAAGTGAGGATTTGGATGGTGGCCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
472 CAAGTGATGATTTGGATGGTGGCCCTACCTGGAGACACGTCTGGCTGACTGGAT-CACAGC 530  
QY 421 AGTGGGGCT 430  
Db ||||||||  
531 AGTGGGGCT 540

RESULT 13  
CA391923 626 bp mRNA linear EST 06-NOV-2002  
LOCUS cs20c09.y1 Human Retinal pigment epithelium/choroid cDNA  
DEFINITION (Un-normalized, unamplified): cs Homo sapiens cDNA clone cs20c09  
5', mRNA sequence.  
CA391923  
CA391923.1 GI:24724221  
EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 626)  
AUTHORS Wistow,G., Bernstein,S.L., Wyatt,M.K., Farris,R.N., Beha,A.,  
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.  
TITLE Expressed sequence tag analysis of human RPE/choroid for the  
NEiBank Project: Over 6000 non-redundant transcripts, novel genes  
and splice variants  
Mol. Vis. 8 (4), 205-220 (2002)  
JOURNAL 22103460  
MEDLINE 12107410  
PUBMED

CONTACT: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA

Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 20 row: C column: 09  
Seq primer: M13RP1 reverse primer (ABI).  
Location/Qualifiers  
1. .626  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="cs20c09"  
/tissue\_type="RPE/choroid"  
/dev\_stage="Adult"  
/lab\_host="EMDH108"  
/clone\_lib="Human Retinal pigment epithelium/choroid cDNA  
(Un-normalized, unamplified): cs"  
/note="Organ: Eye; Vector: pCMVSPORT6; Two different donor  
eyes (75-80 years old) yielded approximately 600 mg of  
dissected RPE/choroid tissue. This in turn yielded 340 ug  
of total RNA and 7 ug of mRNA. A directionally cloned cDNA  
library in the pCMVSPORT6 vector was constructed at Life  
Technologies (Rockville, MD; now part of Invitrogen Corp),  
essentially following the protocols of the SuperScript  
Plasmid System (Invitrogen Corp).  
<http://www.invitrogen.com/>. The library code  
designation was cs. For this library, cDNA inserts were  
cloned into the NotI/MluI sites of the vector. EST  
analysis was performed on the unamplified library at the  
NIH Intramural Sequencing Center (NISC)."

BASE COUNT 108 a 202 c 197 g 118 t 1 others  
ORIGIN

Query Match 67.3%; Score 391.8; DB 14; Length 626;  
Best Local Similarity 91.6%; Pred. No. 2.6e-88;  
Matches 414; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

QY 1 ATGGCGACCCCGAGCTCAACCCCGAGCAAGCTTTGTGGCTGACTTTGTAGGCTAT 60  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
175 ATGGCGACCCCGAGCTCGGCCCGAGCACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 234  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGAGAGCTGGCCCTGGGGAAGGCCCGCCGAC 120  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
235 AAGCTGAGGCAGAGGGTTATGTCTGTGAGAGCTGGCCCGAGGAGGCCCGCCGAGCTGAC 294  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGTAGACCCGTTTCCGCCGACC 180  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
295 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTTCGAGACCCGCTTCCGGCGCACC 354  
QY 181 TTCTCTGACCTGGCCGCTCAGCTACACGTGACCCCGAGCTCAGCCCGAGCAAGCTTCACC 240  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
355 TTCTCTGATCTGGCGGCTCAGCTGCATGTGACCCCGAGGCTCAGCCCAACACGCTTCACC 414  
QY 241 CAGGTTTCCGACGAACCTTTTCCAAAGGGGGCCCTAACTGGGGCGCTTGTGGCATTTCTT 300  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
415 CAGGTTCTCGATGAACCTTTTCAAGGGGGCCCCAACTGGGGCGCCCTTGTAGCCTTCTT 474  
QY 301 GTCTTTGGGCTGCCCTGTGTGTGAGAGTGTCAACAAAGAAATGGAGCCCTTTGGTGGGA 360  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
475 GTCTTTGGGCTGCACCTGTGTGTGAGAGTGTCAACAAAGGAGATGGAACCACTGGTGGGA 534  
QY 361 CAAGTGACGATTTGGATGGTGGCCCTACCTGGAGACACGTCTGGCTGACTGGATCCACAGC 420  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
535 CAAGTGACGAGTGGATGGTGGCCCTACCTGGAGACGCGGCTGGTGGCTGACTGGATCCACAGC 594  
QY 421 AGTGGGGCTGGGGGAGTTTCACAGCTCTATA 452  
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
595 AGTGGGGCTGGGGGAGTTTCACAGCTCTATA 626

RESULT 14  
BI910270 643 bp mRNA linear EST 16-OCT-2001  
LOCUS BI910270  
DEFINITION 603069493F1 NIH\_MGC\_118 Homo sapiens cDNA clone IMAGE:5218294 5',

ACCESSION B1910270  
VERSION B1910270.1 GI:16173653  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (bases 1 to 643)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished  
Contact: Robert Strausberg, Ph.D.  
Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM:1548 row: j column: 23  
High quality sequence stop: 643.  
Location/Qualifiers  
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/clone\_lib="NIH\_MGC\_118"  
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(destroyed); RNA source leukocytes from anonymous pool of  
non-activated adult donors. Library is oligo-dT primed  
and directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.7 kb, insert size range  
1.2-3.3 kb. Library is normalized and enriched for  
full-length clones and was constructed by C. Gruber  
(Invitrogen). Research Genetics tracking code 027. Note:  
this is a NIH\_MGC Library."  
BASE COUNT 129 a 184 c 216 g 114 t  
ORIGIN  
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Best Local Similarity 86.8%; Pred. No. 5.3e-82;  
Matches 415; Conservative 0; Mismatches 62; Indels 1; Gaps 1;  
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Dd 140 ATGGCGACCCAGCCTCGGCCCGAGACACACGGGCTCTGGTGGCAGACTTTGTAGGTTAT 199  
QY 61 AGGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGGCCCGCCGAC 120  
Dd 200 AAGCTGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCGGGAGGGCCCGAGCCTGAC 259  
QY 121 CCGCTGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACC 180  
Dd 260 CCGCTGCACCAAGCCATGCGGGCAGCTGGAGATGAGTTTCGAGACCTCGCTTCCGGCGACC 319  
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Dd 320 TTCTCTGATCTGGCGGCTCAGCTGCATGTACCCCGAGGCTCAGCCCAACACGCTTACC 379  
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Dd 380 CAGGTTCTCCGATGAACCTTTTCAAGGGGGCCCAACTGGGGCGGCTTGTAGCCTTCTT 439  
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Dd 440 GTCTTTGGGGTGCACCTGTGTGCTGAGACTGTCAACAGGAGGATGAACCACTGGTGGG 499  
QY 360 ACAAGTGCAGGATTGGATGGTGGCCCTACCTGGAGACACGCTCTGGCTGACTGGATCCACAG 419

Db 500 ACAAGTGCAGGAGTGGATGGTGGCCTACTGGAGACGGGCTGGCTGACTGGATCCACAG 559  
QY 420 CAGTGGCGGCTGGCGGAGTTTCACAGCTCTATACGGGGACGGGGCCCTGGAGGAGGCA 477  
Dd 560 CAGTGGGGGCTGGGAGCTGGAAGCTATCAAAGCTCGAGTCAGGGAGATGGAGGAAGAA 617  
RESULT 15  
CB749817 440 bp mRNA linear EST 11-APR-2003  
LOCUS AMGNNUC:MRPE3-00122-G12-A placenta embryo D17 (10379) Rattus  
DEFINITION norvegicus cDNA clone mrpe3-00122-g12 5', mRNA sequence.  
ACCESSION CB749817  
VERSION CB749817  
KEYWORDS EST.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 440)  
AUTHORS Amgen EST Program.  
TITLE Amgen Rat EST Program  
JOURNAL Unpublished  
COMMENT Contact: Dan Fitzpatrick  
Amgen, Inc  
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA  
Tel: 805 447-4881  
Plate: 00122 row: g column: 12.  
Location/Qualifiers  
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/note="Vector: pSPOR1; placenta embryo D17"  
BASE COUNT 76 a 113 c 118 g 80 t 53 others  
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Query Match 61.6%; Score 358.4; DB 14; Length 440;  
Best Local Similarity 94.1%; Pred. No. 6.3e-80;  
Matches 368; Conservative 0; Mismatches 23; Indels 0; Gaps 0;  
QY 65 TGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGGCCCGCCGACCCCGC 124  
Dd 50 TGAGGCAGAGGGTTATGTCTGTGAGCTGGCCCTGGGAGAGGCCCGCCGACCCCGC 109  
QY 125 TGCACCAAGCCATGCGGGCTGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCT 184  
Dd 110 TGCACCAAGCCATGCGGGCAGCTGGAGACGAGTTTGAGACCCGTTTCCGCCGCACCTTCT 169  
QY 185 CTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGAGCAGCCTTCAACCCAGG 244  
Dd 170 CTGACCTGGCCGCTCAGCTACACGTGACCCCGAGGCTCAGCCCGAGCAGCCTTCAACCCAGN 229  
QY 245 TTTCCGACGAACCTTTTCCAAGGGGGCCCTAACTGGGGCCGCTTGTGGCATTTCTTTGTCT 304  
Dd 230 TTTCCGACGAACCTTTTCCCGANGGGGGCCCAACTGGGGCCNCTCTTTGTGGCATTTCTTTGTCT 289  
QY 305 TTGGGGTGCCTGTGTGCTGAGAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAG 364  
Dd 290 TTGGGGTGCCTGTGTGCTGANAGTGTCAACAAAGAAATGGAGCCTTTGGTGGGACAAG 349  
QY 365 TGCAGGATTGGATGGTGGCCTACCTGGAGACACGCTCTGGCTGACTGATCCACAGCAGTG 424  
Dd 350 TGCAGGATTGGATGGTGACCTACCTGGAGACACGCTTGGCTGACTGGATCCACAGCANTG 409  
QY 425 GCGGCTGGGGCGGAGTTTCACAGCTCTATACGG 455  
Dd 410 GGGGCTGGGGCGGAGTTTCACAGCTCTATACGG 440



Search completed: October 27, 2003, 13:50:45  
Job time : 1468.74 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:27:45 ; Search time 60 Seconds  
(without alignments)  
510.570 Million cell updates/sec

Title: US-09-925-674A-9

Perfect score: 1009

Sequence: 1 MATPASTPTRALVADFVG.....LTGAVALGALVTVGAFASK 193

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*		
21:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*		
22:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*		
23:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*		
24:	/SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*		

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1006	99.7	193	20 AAY05531	Mouse Bcl-w protei
2	1002	99.3	193	19 AAW61391	Rat bcl-y protein.
3	1002	99.3	193	20 AAW97391	The rat bcl-y prot
4	997	98.8	192	20 AAW97393	Protein sequence o
5	997	98.8	193	20 AAY05530	Human Bcl-w protei
6	992	98.3	193	19 AAW61392	Human bcl-y protei
7	992	98.3	193	20 AAW97392	The human bcl-y pr
8	990	98.1	193	18 AAW36047	Human bcl-w protei
9	990	98.1	193	20 AAY05532	Human Bcl-w protei

10	987	97.8	192	20 AAW97394	Mammalian bcl-y pr
11	970.5	96.2	192	20 AAY05533	Mouse Bcl-w protei
12	879	87.1	168	18 AAW36048	Mouse bcl-w protei
13	811.5	80.4	190	23 AAO18223	Human Bcl-Rambo BH
14	756	74.9	365	19 AAW59884	Amino acid sequenc
15	756	74.9	365	23 ABG59556	Human novel secret
16	429.5	42.6	411	22 AAU00219	Bcl-X1-DTR apoptos
17	427.5	42.4	237	23 ABG78480	Wild type BclXi pr
18	425.5	42.2	233	22 AAB73303	Rat wild-type Bcl-
19	424.5	42.1	233	16 AAR68887	Human thymus BCL-X
20	424.5	42.1	233	17 AAW05821	Bcl-XL protein. H
21	424.5	42.1	233	18 AAW31530	Human anti-apoptot
22	424.5	42.1	233	21 AAY83223	Bcl-x polypeptide.
23	424.5	42.1	233	21 AAY69969	Human Bcl-XL prote
24	424.5	42.1	233	22 AAG64262	Human Bcl-XL prote
25	424.5	42.1	233	22 AAB50538	Human Bcl-XL prote
26	424.5	42.1	233	22 AAB47515	Protein encoded by
27	422	41.8	225	18 AAW19396	"Deprenyl" (RTM)-1
28	421.5	41.8	233	22 AAB73304	Mutant rat Bcl-XL
29	412.5	40.9	239	22 AAG64037	Human Bcl-2 protei
30	411.5	40.8	152	24 AAG79760	Bcl-XL. Homo sapi
31	409	40.5	236	22 AAB35131	Murine Bcl-2. Mus
32	409	40.5	236	23 AAU76554	Murine Bcl-2 polyp
33	408.5	40.5	239	20 AAW87810	A human Bcl-2 prot
34	408.5	40.5	239	22 AAB74127	Human bcl-2. Homo
35	408.5	40.5	239	22 AAB35130	Human Bcl-2. Homo
36	408.5	40.5	239	23 ABG78478	Human Bcl2 mutant
37	408.5	40.5	239	23 ABG78479	Human Bcl-2 polype
38	408.5	40.5	239	23 AAU76553	Human DITHP cell m
39	408.5	40.5	272	24 ABR41675	Sequence of bcl-2-
40	406.5	40.3	239	9 AAP80987	Bcl-2 oncogene pro
41	406.5	40.3	239	14 AAR42312	Human bcl-2 protei
42	406.5	40.3	239	16 AAR70331	Human bcl-2 alpha
43	406.5	40.3	239	16 AAR71404	Human bcl-2. Homo
44	406.5	40.3	239	19 AAW40217	Human bcl-2. Homo
45	406.5	40.3	239	20 AAW87812	A human Bcl-2-alph

ALIGNMENTS

RESULT 1	
AAY05531	
ID	AAY05531 standard; Protein; 193 AA.
XX	
AC	AAY05531;
XX	
DT	05-JUL-1999 (first entry)
XX	
DE	Mouse Bcl-w protein essential for spermatogenesis.
XX	
KW	Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;
KW	animal model.
XX	
OS	Mus sp.
XX	
PN	WO9913710-A1.
XX	
PD	25-MAR-1999.
XX	
PF	16-SEP-1998; 98WO-AU00764.
XX	
PR	16-SEP-1997; 97AU-0009228.
XX	
PA	(HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
XX	
PI	Adams J, Cory S, Gibson L, Koentgen F, Print C;
XX	
DR	WPI; 1999-243890/20.
DR	N-PSDB; AAX25133.
XX	
PT	An animal model exhibiting reduced levels of a Bcl-w protein and/or protein associated with Bcl-w

XX	Claim 2; Page 35; 52pp; English.	PT	Nucleic acids encoding B-cell lymphoma-γ protein - useful for producing recombinant protein for use in treating uncontrolled cell growth e.g. cancers		
PS		PT			
XX		XX			
CC	The present sequence is mouse Bcl-w, a pro-survival member of the Bcl-2 family which is widely expressed and which is essential for spermatogenesis. The invention relates generally to a method of treatment and to an animal model for the identification of molecules and genetic sequences useful for inducing or reducing fertility of male animals. Methods are provided for the treatment of infertility, or for reducing fertility, by modulating spermatogenesis. An animal model carries a mutation is at least one allele of the human or murine bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w. Such animals have disorganised seminiferous tubules and are substantially infertile, but possess no other major abnormalities as determined by histological examination. They can be used to screen for therapeutic molecules including genetic sequences capable of inducing, enhancing or otherwise facilitating spermatogenesis in animals, or which can induce infertility.	XX	Example; Fig 3A; 27pp; English.		
XX		PS	The mammalian bcl-y protein is a member of the bcl-2 family, components in the cell death pathway. The bcl-2 family have both apoptotic activity and the apoptosis blocking activity. bcl-y falls in the apoptosis activity category. The recombinant protein may be used to prevent uncontrolled cell growth, either by its direct administration to recombinant genetic constructs to increase its expression in vivo. Also, antisense constructs can be used in disorders where prevention of cell death is desired.	XX	
SQ	Sequence 193 AA;	SQ	Sequence 193 AA;		
	Query Match 99.7%; Score 1006; DB 20; Length 193; Best Local Similarity 99.5%; Pred. No. 7e-102; Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;		Query Match 99.3%; Score 1002; DB 19; Length 193; Best Local Similarity 99.0%; Pred. No. 1.9e-101; Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;		
QY	1 MATPASTPTDTRALVADFVGYLRLQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60	QY	1 MATPASTPTDTRALVADFVGYLRLQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60		
DB	1 MATPASTPTDTRALVADFVGYLRLQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60	DB	1 MATPASTPTDTRALVADFVGYLRLQKGYVCGAGPGEPAADPLHQAMRAAGDEFETRFRRT 60		
QY	61 FSDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120	QY	61 FSDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120		
DB	61 FSDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120	DB	61 FSDLAALQHLVTPGSAQQRFTQVSDQLFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120		
QY	121 QVQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRGNWASVRTVLTGAVAL 180	QY	121 QVQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRGNWASVRTVLTGAVAL 180		
DB	121 QVQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRGNWASVRTVLTGAVAL 180	DB	121 QVQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARRLRGNWASVRTVLTGAVAL 180		
QY	181 GALVTVGAFFASK 193	QY	181 GALVTVGAFFASK 193		
DB	181 GALVTVGAFFASK 193	DB	181 GALVTVGAFFASK 193		
RESULT 2		RESULT 3			
AAW61391		AAW97391			
ID	AAW61391 standard; Protein; 193 AA.	ID	AAW97391 standard; Protein; 193 AA.		
XX		XX			
AC	AAW61391;	AC	AAW97391;		
XX		XX			
DT	02-OCT-1998 (first entry)	DT	20-MAY-1999 (first entry)		
XX		XX			
DE	Rat bcl-y protein.	DE	The rat bcl-y protein.		
XX		XX			
KW	bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; rat.	KW	Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue; programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke; head trauma; Alzheimer's Disease; neural; muscular degenerative disease; multiple sclerosis; myocardial infarction; vitally induced cell death; aging; spinal cord injury; amyotrophic lateral sclerosis; cancer; premature cell death; cell death stimulator; prolonged cell life span; Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease; parasite.		
OS	Rattus sp.	OS	Rattus sp.		
XX		XX			
PN	US5789201-A.	PN	US5883229-A.		
XX		XX			
PD	04-AUG-1998.	PD	16-MAR-1999.		
XX		XX			
PF	11-FEB-1997; 97US-0798897.	PF	25-NOV-1997; 97US-0978523.		
XX		XX			
PR	23-FEB-1996; 96US-0012201.	PR	23-FEB-1996; 96US-0012201.		
PR	11-FEB-1997; 97US-0798897.	PR	11-FEB-1997; 97US-0798897.		
XX		PR	25-NOV-1997; 97US-0978523.		
XX	(COCE-) COGENSYS INC.	XX			
PA	Guastella J;	PA	(COCE-) COGENSYS INC.		
PI		PI	Guastella J;		
XX		XX			
DR	WPI; 1998-446079/38.	XX			
DR	N-PSDB; AAV28333.	XX			
XX		XX			

DR WPI; 1999-214150/18.  
DR N-PSDB; AAX15945.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
PT for modulating programmed cell death  
XX  
PS Disclosure; Columns 15-18; 26pp; English.  
XX  
CC The present sequence represents rat bcl-y protein (Rbcl-y). The  
CC specification also describes human bcl-y protein (Hbcl-y). Rbcl-y and  
CC Hbcl-y are homologues of the bcl-2 protein thought to be involved in  
CC programmed cell death (apoptosis and necrosis). Rbcl-y and Hbcl-y  
CC proteins may be used to treat conditions associated with a disruption of  
CC the cell death pathway. If they act as cell death inhibitors, they may be  
CC used in therapies to treat subjects suffering from: strokes, head trauma,  
CC Alzheimer's Disease, neural and muscular degenerative diseases  
CC (especially multiple sclerosis), myocardial infarction, vitally induced  
CC cell death, aging, spinal cord injuries and amyotrophic lateral  
CC sclerosis- conditions where cells under go premature cell death as a  
CC result of triggers which may or may not be apparent. They may also be  
CC used in this way to develop cell lines which remain viable in culture for  
CC an extended period. In contrast, if they act as cell death stimulators,  
CC Rbcl-y and Hbcl-y may be used to treat conditions associated with  
CC prolonged cell life span such as cancer (especially kaposi's sarcoma and  
CC lung cancer) and auto/hyperimmune diseases. They may also be used to  
CC cause cell death in, and hence control, parasites.  
XX  
SQ Sequence 193 AA;  
Query Match 99.3%; Score 1002; DB 20; Length 193;  
Best Local Similarity 99.0%; Pred. No. 1.9e-101;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASTPDTRALVADFVGYYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASTPDTRALVADFVGYYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGPSAQQRFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAQLHVTGPSAQQRFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMVYVLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVAL 180  
Db 121 QVQDMVYVLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVAL 180  
QY 181 GALVTVGAFPAASK 193  
Db 181 GALVTVGAFPAASK 193  
RESULT 4  
AAW97393  
ID AAW97393 standard; Protein; 192 AA.  
XX  
AC AAW97393;  
XX  
DT 20-MAY-1999 (first entry)  
XX  
DE Protein: sequence of the specification.  
XX  
KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;  
KW premature cell death; cell death stimulator; prolonged cell life span;  
KW Kaposi's sarcoma; lung cancer; autoimmune; hyperimmune disease;  
KW parasite.  
XX  
OS Unidentified.  
XX  
PN US5883229-A.  
XX

PD 16-MAR-1999.  
XX  
PF 25-NOV-1997; 97US-0978523.  
XX  
PR 23-FEB-1996; 96US-0012201.  
PR 11-FEB-1997; 97US-0798897.  
PR 25-NOV-1997; 97US-0978523.  
XX  
PA (COCE-) COCENSYS INC.  
XX  
PI Guastelia J;  
XX  
DR WPI; 1999-214150/18.  
XX  
PT Novel bcl-y homologues of the rat and human bcl-2 protein - useful  
PT for modulating programmed cell death  
XX  
PS Disclosure; Columns 19-20; 26pp; English.  
XX  
CC The specification describes rat bcl-y protein (Rbcl-y) and human bcl-y  
CC protein (Hbcl-y). Rbcl-y and Hbcl-y are homologues of the bcl-2 protein  
CC thought to be involved in programmed cell death (apoptosis and necrosis).  
CC Rbcl-y and Hbcl-y proteins may be used to treat conditions associated  
CC with a disruption of the cell death pathway. If they act as cell death  
CC inhibitors, they may be used in therapies to treat subjects suffering  
CC from: strokes, head trauma, Alzheimer's Disease, neural and muscular  
CC degenerative diseases (especially multiple sclerosis), myocardial  
CC infarction, vitally induced cell death, aging, spinal cord injuries and  
CC amyotrophic lateral sclerosis- conditions where cells under go premature  
CC cell death as a result of triggers which may or may not be apparent.  
CC They may also be used in this way to develop cell lines which remain  
CC viable in culture for an extended period. In contrast, if they act as  
CC cell death stimulators, Rbcl-y and Hbcl-y may be used to treat  
CC conditions associated with prolonged cell life span such as cancer  
CC (especially kaposi's sarcoma and lung cancer) and auto/hyperimmune  
CC diseases. They may also be used to cause cell death in, and hence  
CC control, parasites.  
XX  
SQ Sequence 192 AA;  
Query Match 98.8%; Score 997; DB 20; Length 192;  
Best Local Similarity 99.0%; Pred. No. 6.7e-101;  
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ATPASTPDTRALVADFVGYYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61  
Db 1 ATPASTPDTRALVADFVGYYKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAQLHVTGPSAQQRFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 121  
Db 61 SDLAQLHVTGPSAQQRFTQVSDSELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 120  
QY 122 VQDMVYVLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALG 181  
Db 121 VQDMVYVLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALG 180  
QY 182 ALVTVGAFPAASK 193  
Db 181 ALVTVGAFPAASK 192  
RESULT 5  
AAW97393  
ID AAW97393 standard; Protein; 193 AA.  
XX  
AC AAW97393;  
XX  
DT 05-JUL-1999 (first entry)  
XX  
DE Human Bcl-w protein essential for spermatogenesis.  
XX  
KW Spermatogenesis; Bcl-3; Bcl-2; human; fertility; infertility;  
KW animal model.



XX OS Homo sapiens.  
XX PN WO9913710-A1.  
XX PD 25-MAR-1999.  
XX PF 16-SEP-1998; 98WO-AU00764.  
XX PR 16-SEP-1997; 97AU-0009228.  
XX PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
XX PI Adams J, Cory S, Gibson L, Koentgen F, Print C;  
XX WPI; 1999-243890/20.  
XX DR N-PSDB; AAX25132.  
XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
XX protein associated with Bcl-w  
XX Claim 2; Page 33; 52pp; English.  
XX The present sequence is human Bcl-w, a pro-survival member of the  
XX Bcl-2 family which is widely expressed and which is essential for  
XX spermatogenesis. The invention relates generally to a method of  
XX treatment and to an animal model for the identification of  
XX molecules and genetic sequences useful for inducing or reducing  
XX fertility of male animals. Methods are provided for the treatment  
XX of infertility, or for reducing fertility, by modulating  
XX spermatogenesis. An animal model carries a mutation is at least  
XX one allele of the human or murine bcl-w gene (see AAX25132-35) or in  
XX a gene associated with bcl-w. Such animals have disorganised  
XX seminiferous tubules and are substantially infertile, but possess no  
XX other major abnormalities as determined by histological examination.  
XX They can be used to screen for therapeutic molecules including  
XX genetic sequences capable of inducing, enhancing or otherwise  
XX facilitating spermatogenesis in animals, or which can induce  
XX infertility.

XX Sequence 193 AA;

Query Match 98.8%; Score 997; DB 20; Length 193;  
Best Local Similarity 98.4%; Pred. No. 6.8e-101;  
Matches 190; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFVGYYLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFVGYYLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHVTTPGSAQQRFQVSDELFGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQLHVTTPGSAQQRFQVSDELFGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
DB 121 QVQEWVWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
QY 181 GALVTVGGAFFASK 193  
DB 181 GALVTVGGAFFASK 193

RESULT 6  
AAW61392  
ID AAW61392 standard; Protein; 193 AA.  
XX AC AAW61392;  
XX XX  
DT 02-OCT-1998 (first entry)  
XX XX  
DE Human bcl-y protein.  
XX XX

KW bcl-y; bcl-2; cell death pathway; apoptotic; apoptosis; human.  
XX OS Homo sapiens.  
XX PN US5789201-A.  
XX PD 04-AUG-1998.  
XX PF 11-FEB-1997; 97US-0798897.  
XX PR 23-FEB-1996; 96US-0012201.  
XX PR 11-FEB-1997; 97US-0798897.  
XX PA (COCE-) COCENSYS INC.  
XX PI Guastella J;  
XX WPI; 1998-446079/38.  
XX DR N-PSDB; AAV28334.  
XX Nucleic acids encoding B-cell lymphoma-y protein - useful for  
XX producing recombinant protein for use in treating uncontrolled cell  
XX growth e.g. cancers  
XX Example; Column 17/18; 27pp; English.  
XX The mammalian bcl-y protein is a member of the bcl-2 family, components  
XX in the cell death pathway. The bcl-2 family have both apoptotic activity  
XX and the apoptosis blocking activity. bcl-y falls in the apoptosis  
XX activity category. The recombinant protein may be used to prevent  
XX uncontrolled cell growth, either by its direct administration to  
XX recombinant genetic constructs to increase its expression in vivo. Also,  
XX antisense constructs can be used in disorders where prevention of cell  
XX death is desired.  
XX Sequence 193 AA;

Query Match 98.3%; Score 992; DB 19; Length 193;  
Best Local Similarity 97.9%; Pred. No. 2.4e-100;  
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MATPASTPTDTRALVADFVGYYLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFVGYYLRQKGYVCGAGPGEGPAADPLHQAAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQLHVTTPGSAQQRFQVSDELFGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQLHVTTPGSAQQRFQVSDELFGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
DB 121 QVQEWVWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
QY 181 GALVTVGGAFFASK 193  
DB 181 GALVTVGGAFFASK 193

RESULT 7  
AAW97392  
ID AAW97392 standard; Protein; 193 AA.  
XX AC AAW97392;  
XX XX  
DT 20-MAY-1999 (first entry)  
XX XX  
DE The human bcl-y protein.

KW Rat bcl-y protein; Rbcl-y; human bcl-y protein; Hbcl-y; bcl-2 homologue;  
KW programmed cell death; apoptosis; necrosis; cell death inhibitor; stroke;  
KW head trauma; Alzheimer's Disease; neural; muscular degenerative disease;  
KW multiple sclerosis; myocardial infarction; vitally induced cell death;  
KW aging; spinal cord injury; amyotrophic lateral sclerosis; cancer;





QY 122 VQDWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTLVTGVALG 181  
Dd 121 VQEWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTLVTGVALG 180  
QY 182 ALVTVGAFASK 193  
Dd 181 ALVTVGAFASK 192

RESULT 11  
AAAY05533  
ID AAY05533 standard; Protein; 192 AA.

AC AAY05533;  
DT 05-JUL-1999 (first entry)  
XX Mouse Bcl-w protein derivative.  
DE Spermatogenesis; Bcl-3; Bcl-2; mouse; fertility; infertility;  
KW animal model.  
XX Mus sp.

OS WO9913710-A1.  
XX 25-MAR-1999.  
PD 16-SEP-1998; 98WO-AU00764.  
XX 16-SEP-1997; 97AU-0009228.  
XX (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.  
PA Adams J, Cory S, Gibson L, Koentgen F, Print C;  
XX WPI; 1999-243890/20.  
DR N-PSDB; AAX25135.

XX An animal model exhibiting reduced levels of a Bcl-w protein and/or  
PT protein associated with Bcl-w

XX Disclosure; Page 39; 52pp; English.

XX The present sequence is described of a derivative of mouse Bcl-w  
CC (see also AAY05531), a pro-survival member of the Bcl-2 family that  
CC is widely expressed, and which is essential for spermatogenesis.  
CC The derivative lacks the 24 N-terminal amino acids of Bcl-w.  
CC The invention relates generally to a method of treatment and to an  
CC animal model for the identification of molecules and genetic  
CC sequences useful for inducing or reducing fertility of male animals.  
CC Methods are provided for the treatment of infertility, or for  
CC reducing fertility, by modulating spermatogenesis. An animal model  
CC carries a mutation is at least one allele of the human or murine  
CC bcl-w gene (see AAX25132-35) or in a gene associated with bcl-w.  
CC Such animals have disorganised seminiferous tubules and are  
CC substantially infertile, but possess no other major abnormalities  
CC as determined by histological examination. They can be used to  
CC screen for therapeutic molecules including genetic sequences  
CC capable of inducing, enhancing or otherwise facilitating  
CC spermatogenesis in animals, or which can induce infertility.

SQ Sequence 192 AA;  
Query Match 96.2%; Score 970.5; DB 20; Length 192;  
Best Local Similarity 96.4%; Pred. NO. 5.4e-98;  
Matches 186; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 MATPASTPDTRALVADFVGRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
Dd 1 MPTPASTPDTRALVADFVGRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTFGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120

Dd 61 FSDLAAQLHVTFGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTLVTGVALG 180  
Dd 121 QVQDWIVAYLETRLADWIHSSGGWADFTALYGDGALEDARRRLREGNWA-VSTVVTGVAL 179  
QY 181 GALVTVGAFASK 193  
Dd 180 GALVTVGAFASK 192

RESULT 12  
AAW36048  
ID AAW36048 standard; Protein; 168 AA.

XX AAW36048;  
AC AAW36048;  
DT 22-APR-1998 (first entry)  
XX Mouse bcl-w protein.  
DE Bcl-w; apoptosis; bcl-2; cell survival; treatment; therapy; cancer;  
KW diagnosis; degenerative disease.  
XX Mus sp.

OS WO9735971-A1.  
XX 02-OCT-1997.  
XX 27-MAR-1997; 97WO-AU00199.  
PR 27-MAR-1996; 96AU-0008965.  
XX (AMRA-) AMRAD OPERATIONS PTY LTD.

PA Adams JM, Cory S, Gibson LM, Holmgreen SP;  
PI WPI; 1997-489635/45.  
XX N-PSDB; AAT96578.

XX Nucleic acid encoding apoptosis related gene bcl-w - used to induce  
PT or inhibit cell survival, e.g. for treatment of cancer and  
PT degenerative diseases

PS Claim 6; Page 50-51; 86pp; English.

XX This sequence represents a novel protein, bcl-w, encoded by the mouse  
CC bcl-2 gene family. This gene promotes cell survival, so its modulation  
CC is useful in treatment of cancer or auto-immune diseases, degenerative  
CC diseases (e.g. stroke, Alzheimer's disease, myocardial infarct, muscular  
CC degeneration, hypoxia, ischaemia, human immunodeficiency virus infection  
CC or in cell transplants. Up-regulation of the gene can also be used to  
CC modify cell lines cultured in vivo, e.g. to develop new lines, to  
CC facilitate isolation of hybridomas and to increase survival of primary  
CC explants during genetic modification. It can be used to produce  
CC recombinant Bcl-w for therapy, diagnosis, antibody production or  
CC screening of potential modulators.

SQ Sequence 168 AA;  
Query Match 87.1%; Score 879; DB 18; Length 168;  
Best Local Similarity 97.6%; Pred. NO. 4.8e-88;  
Matches 164; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

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Dd 1 MPTPASTPDTRALVADFVGRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTFGSAQQRFTQVSDSELFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120  
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ABG95556  
ID ABG95556 standard; Protein; 365 AA.  
XX  
AC ABG95556;  
XX  
DT 15-JAN-2003 (first entry)  
DE Human novel secreted protein gene l20 polypeptide #1.  
XX  
KW Human; secreted protein; autoimmune disease; chemotaxis;  
KW rheumatoid arthritis; hyperproliferative disorder; breast neoplasia;  
KW liver neoplasm cardiovascular disorder; cardiac arrest; skin aging;  
KW cerebrovascular disorders; cerebral ischaemia; angiogenesis; sunburn;  
KW nervous system disorders; Alzheimer's disease; infection;  
KW ocular disorder; corneal infection; wound healing; tissue regeneration;  
KW epithelial cell proliferation; organ transplantation; food additive;  
KW preservative; nutritional.  
XX  
OS Homo sapiens.  
XX  
PN US6420526-B1.  
XX  
PD 16-JUL-2002.  
XX  
PF 08-SEP-1998; 98US-0149476.  
XX  
PR 07-MAR-1997; 97US-038621P.  
PR 07-MAR-1997; 97US-040161P.  
PR 07-MAR-1997; 97US-040162P.  
PR 07-MAR-1997; 97US-040163P.  
PR 07-MAR-1997; 97US-040333P.  
PR 07-MAR-1997; 97US-040334P.  
PR 07-MAR-1997; 97US-040336P.  
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PR 23-MAY-1997; 97US-047492P.  
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PR 23-MAY-1997; 97US-047501P.  
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PR 23-MAY-1997; 97US-047598P.  
PR 23-MAY-1997; 97US-047599P.  
PR 23-MAY-1997; 97US-047600P.

PR 23-MAY-1997; 97US-047601P.  
PR 23-MAY-1997; 97US-047612P.  
PR 23-MAY-1997; 97US-047613P.  
PR 23-MAY-1997; 97US-047614P.  
PR 23-MAY-1997; 97US-047615P.  
PR 23-MAY-1997; 97US-047617P.  
PR 23-MAY-1997; 97US-047618P.  
PR 23-MAY-1997; 97US-047632P.  
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PR 06-JUN-1997; 97US-048964P.  
PR 06-JUN-1997; 97US-048974P.  
PR 13-JUN-1997; 97US-049610P.  
PR 08-JUL-1997; 97US-051926P.  
PR 16-JUL-1997; 97US-052874P.  
PR 18-AUG-1997; 97US-055724P.  
PR 22-AUG-1997; 97US-056630P.  
PR 22-AUG-1997; 97US-056631P.  
PR 22-AUG-1997; 97US-056632P.  
PR 22-AUG-1997; 97US-056636P.  
PR 22-AUG-1997; 97US-056637P.  
PR 22-AUG-1997; 97US-056662P.  
PR 22-AUG-1997; 97US-056664P.  
PR 22-AUG-1997; 97US-056845P.  
PR 22-AUG-1997; 97US-056862P.  
PR 22-AUG-1997; 97US-056864P.  
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PR 22-AUG-1997; 97US-056874P.  
PR 22-AUG-1997; 97US-056875P.  
PR 22-AUG-1997; 97US-056876P.  
PR 22-AUG-1997; 97US-056877P.  
PR 22-AUG-1997; 97US-056878P.  
PR 22-AUG-1997; 97US-056879P.  
PR 22-AUG-1997; 97US-056880P.  
PR 22-AUG-1997; 97US-056881P.  
PR 22-AUG-1997; 97US-056882P.  
PR 22-AUG-1997; 97US-056884P.  
PR 22-AUG-1997; 97US-056886P.  
PR 22-AUG-1997; 97US-056887P.  
PR 22-AUG-1997; 97US-056888P.  
PR 22-AUG-1997; 97US-056889P.  
PR 22-AUG-1997; 97US-056892P.  
PR 22-AUG-1997; 97US-056893P.  
PR 22-AUG-1997; 97US-056894P.  
PR 22-AUG-1997; 97US-056903P.  
PR 22-AUG-1997; 97US-056908P.  
PR 22-AUG-1997; 97US-056909P.  
PR 22-AUG-1997; 97US-056910P.  
PR 22-AUG-1997; 97US-056911P.  
PR 22-AUG-1997; 97US-057761P.  
PR 05-SEP-1997; 97US-057650P.  
PR 05-SEP-1997; 97US-057669P.  
PR 12-SEP-1997; 97US-058785P.  
PR 02-OCT-1997; 97US-061060P.  
PR 06-MAR-1998; 98WO-JS04493.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Rosen CA, Fischer CL, Soppet DP, Carter KC, Bednarik DR;  
PI Endress GA, Yu G, Ni J, Feng P, Young PE, Greene JM, Ferrie AM;  
PI Duan R, Hu J, Florence KA, Olsen HS, Ebner R, Brewer LA;  
PI Moore PA, Shi Y, Lafleur DW, Li Y, Zeng Z, Kyaw H;  
XX  
DR WPI; 2002-634796/68.  
XX  
PT New isolated human secreted protein for diagnosing, preventing,  
PT treating or ameliorating medical conditions and used as a food additive  
PT or preservative -  
XX  
PS Disclosure; Column 103; 129pp; English.  
XX  
CC The invention relates to an isolated protein that is one of 186 human  
CC secreted proteins, given in the specification, encoded by one of  
CC 309 cDNA sequences also given in the specification. The protein is used



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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:46:25 ; Search time 21 Seconds  
(without alignments)  
388.857 Million cell updates/sec

Title: US-09-925-674A-9  
Perfect score: 1009  
Sequence: 1 MATPASTPDTRALVADFVGY.....LTGAVALGALVTVGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	1002	99.3	193	2	US-08-978-523-3
3	997	98.8	192	1	US-08-798-897-5
4	997	98.8	192	2	US-08-978-523-5
5	992	98.3	193	1	US-08-798-897-4
6	992	98.3	193	2	US-08-978-523-4
7	987	97.8	192	1	US-08-798-897-6
8	987	97.8	192	2	US-08-978-523-6
9	756	74.9	365	4	US-09-149-476-696
10	425.5	42.2	233	4	US-09-271-014A-6
11	424.5	42.1	233	1	US-08-333-565-59
12	424.5	42.1	233	1	US-08-081-448-6
13	424.5	42.1	233	1	US-08-607-269-24
14	424.5	42.1	233	1	US-08-471-058-14
15	424.5	42.1	233	2	US-08-663-479-59
16	424.5	42.1	233	2	US-08-470-670A-7
17	424.5	42.1	233	3	US-08-471-057-14
18	424.5	42.1	233	3	US-08-481-739-2
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22	424.5	42.1	233	4	US-08-470-865-14
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26	420.5	41.7	233	1	US-08-607-269-23
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28	409	40.5	236	1	US-08-607-269-22	Sequence 22, Appl
29	409	40.5	236	3	US-09-127-048-9	Sequence 9, Appl
30	409	40.5	236	5	PCT-US95-04600-22	Sequence 22, Appl
31	408.5	40.5	239	1	US-08-112-208C-10	Sequence 10, Appl
32	408.5	40.5	239	1	US-08-248-819A-1C	Sequence 10, Appl
33	408.5	40.5	239	2	US-08-337-646A-10	Sequence 10, Appl
34	408.5	40.5	239	2	US-08-856-531-10	Sequence 10, Appl
35	408.5	40.5	239	2	US-08-856-034-10	Sequence 10, Appl
36	408.5	40.5	239	3	US-09-127-048-8	Sequence 8, Appl
37	408.5	40.5	239	3	US-08-927-326-10	Sequence 10, Appl
38	408.5	40.5	239	4	US-09-379-820A-10	Sequence 10, Appl
39	406.5	40.3	239	1	US-08-333-565-51	Sequence 51, Appl
40	406.5	40.3	239	1	US-08-248-819A-12	Sequence 12, Appl
41	406.5	40.3	239	1	US-08-607-269-20	Sequence 20, Appl
42	406.5	40.3	239	1	US-08-471-059-12	Sequence 12, Appl
43	406.5	40.3	239	1	US-08-690-095-4	Sequence 4, Appl
44	406.5	40.3	239	2	US-08-465-485A-21	Sequence 21, Appl
45	406.5	40.3	239	2	US-08-661-479-51	Sequence 51, Appl

ALIGNMENTS

RESULT 1  
US-08-798-897-3  
; Sequence 3, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-Y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-3

Query Match 99.3%; Score 1002; DB 1; Length 193;  
Best Local Similarity 99.0%; Pred. No. 3.3e-106;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
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DB 1 MATPASTPDTRALVADFVGYKLQKGYVCGAGPGEGPAADPLHQAMPAAGDEFETRFRRT 60  
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QY 61 FSLAAQLHVTPTGSAQQRFTQVSDQLFQGGPNWGRLLVAFVFGAALCAESVNKEMEPLVG 120



Db 61 FSDLAQLHVTGPSAQQRFTQVSDLEFQGGPNWGRLLVAFVFGAALCAESVKNEMEPLVG 120  
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Db 121 QVQDMWVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180  
Qy 181 GALVTVGGAFFASK 193  
Db 181 GALVTVGGAFFASK 193

RESULT 2  
US-08-978-523-3  
; Sequence 3, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DCS  
; SOFTWARE: Patent-In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith  
; CLASSIFICATION: 424  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 193 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-978-523-3

Query Match 99.3%; Score 1002; DB 2; Length 193;  
Best Local Similarity 99.0%; Pred. No. 3.3e-106;  
Matches 191; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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Db 1 MATPASTPDTRALVADFVGYYKLQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
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Db 121 QVQDMWVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL 180

Qy 181 GALVTVGGAFFASK 193  
Db 181 GALVTVGGAFFASK 193  
RESULT 3  
US-08-798-897-5  
; Sequence 5, Application US/08798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; TITLE OF INVENTION: Homologue  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent-In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/798,897  
; FILING DATE: February 11, 1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Esmond, Robert W.  
; REGISTRATION NUMBER: 32,893  
; REFERENCE/DOCKET NUMBER: 1483.0140001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-371-2600  
; TELEFAX: 202-371-2540  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 192 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-798-897-5

Query Match 98.8%; Score 997; DB 1; Length 192;  
Best Local Similarity 99.0%; Pred. No. 1.2e-105;  
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
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Qy 62 SDLAALHVTGPSAQQRFTQVSDLEFQGGPNWGRLLVAFVFGAALCAESVKNEMEPLVGQ 121  
Db 61 SDLAALHVTGPSAQQRFTQVSDLEFQGGPNWGRLLVAFVFGAALCAESVKNEMEPLVGQ 120  
Qy 122 VQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALG 181  
Db 121 VQDMWVTYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVALG 180  
Qy 182 ALVTVGGAFFASK 193  
Db 181 ALVTVGGAFFASK 192

RESULT 4  
US-08-978-523-5  
; Sequence 5, Application US/08978523  
; Patent No. 5883229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John

;; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
;; TITLE OF INVENTION: Homologue  
;; NUMBER OF SEQUENCES: 53  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
;; STREET: 1100 New York Avenue, N.W., Suite 600  
;; CITY: Washington  
;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/978,523  
;; FILING DATE: herewith  
;; CLASSIFICATION: 424  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 08/798,897  
;; FILING DATE: February 11, 1997  
;; CLASSIFICATION: 424  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1483.0140002  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 5:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 192 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-978-523-5  
Query Match 98.8%; Score 997; DB 2; Length 192;  
Best Local Similarity 99.0%; Pred. No. 1.2e-105;  
Matches 190; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 2 ATPASTPTDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 61  
DB 1 ATPASTPTDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAAQLHVTTPGSAQORFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNKEMEPLVGQ 121  
DB 61 SDLAAQLHVTTPGSAQORFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNKEMEPLVGQ 120  
QY 122 VQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALG 181  
DB 121 VQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALG 180  
QY 182 ALVTVGAFVASK 193  
DB 181 ALVTVGAFVASK 192  
RESULT 5  
US-08-798-897-4  
; Sequence 4, Application US/08/798897  
; Patent No. 5789201  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington

;; STATE: DC  
;; COUNTRY: USA  
;; ZIP: 20005  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: Patent In Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/798,897  
;; FILING DATE: February 11, 1997  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Esmond, Robert W.  
;; REGISTRATION NUMBER: 32,893  
;; REFERENCE/DOCKET NUMBER: 1483.0140001  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 202-371-2600  
;; TELEFAX: 202-371-2540  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 193 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: not relevant  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-798-897-4  
Query Match 98.3%; Score 992; DB 1; Length 193;  
Best Local Similarity 97.9%; Pred. No. 4.5e-105;  
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASTPTDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASTPTDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAAQLHVTTPGSAQORFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNKEMEPLVG 120  
DB 61 FSDLAAQLHVTTPGSAQORFTQVSDDELFGGPNWGRLVAFVFGAALCAESVKNKEMEPLVG 120  
QY 121 VQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVAL 180  
DB 121 VQDMVMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVAL 180  
QY 181 GALVTVGAFVASK 193  
DB 181 GALVTVGAFVASK 193  
RESULT 6  
US-08-978-523-4  
; Sequence 4, Application US/08/978523  
; Patent No. 5893229  
; GENERAL INFORMATION:  
; APPLICANT: Guastella, John  
; TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
; NUMBER OF SEQUENCES: 53  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
; STREET: 1100 New York Avenue, N.W., Suite 600  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/978,523  
; FILING DATE: herewith

CLASSIFICATION: 424  
PRIOR APPLICATION DATA: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 193 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-978-523-4

Query Match 98.3%; Score 992; DB 2; Length 193;  
Best Local Similarity 97.9%; Pred. No. 4.5e-105;  
Matches 189; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 1 MATPASTPDTRALVADFVGRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
Db 1 MATPASAPDTRALVEDFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAQLHVTGSAQQRFTQVSDLELFGGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120  
Db 61 FSDLAQLHVTGSAQQRFTQVSDLELFGGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQNMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARLRREGNWSVRTVLTGAVAL 180  
Db 121 QVQNMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARLRREGNWSVRTVLTGAVAL 180  
QY 181 GALVTGGAFFASK 193  
Db 181 GALVTGGAFFASK 193

RESULT 7  
US-08-978-897-6  
Sequence 6, Application US/08798897  
Patent No. 5789201  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-798-897-6

Query Match 97.8%; Score 987; DB 1; Length 192;  
Best Local Similarity 97.9%; Pred. No. 1.7e-104;  
Matches 188; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
QY 2 ATPASTPDTRALVADFVGRLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 61  
Db 1 ATPASAPDTRALVEDFVGKLRQKGYVCGAGPGGPAADPLHQAMRAAGDEFETRFRRTF 60  
QY 62 SDLAQLHVTGSAQQRFTQVSDLELFGGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 121  
Db 61 SDLAQLHVTGSAQQRFTQVSDLELFGGGPNWGRVLVAFVFGAALCAESVNKEMEPLVG 120  
QY 122 VQDMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARLRREGNWSVRTVLTGAVALG 181  
Db 121 VQDMVAYLETRLADWIHSSGGWAEFTALYGDGALAEARLRREGNWSVRTVLTGAVALG 180  
QY 182 ALVTGGAFFASK 193  
Db 182 ALVTGGAFFASK 192

RESULT 8  
US-08-978-523-6  
Sequence 6, Application US/08978523  
Patent No. 5883229  
GENERAL INFORMATION:  
APPLICANT: Guastella, John  
TITLE OF INVENTION: Genes Coding For Bcl-y, a Bcl-2  
TITLE OF INVENTION: Homologue  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 New York Avenue, N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/978,523  
FILING DATE: herewith  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/798,897  
FILING DATE: February 11, 1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1483.0140002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 192 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear

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; MOLECULE TYPE: protein
; US-08-978-523-6
; Query Match 97.8%; Score 987; DB 2; Length 192;
; Best Local Similarity 97.9%; Fred.No. 1.7e-104;
; Matches 188; Conservative 2; Mismatches 2; Indels 0; Gaps 3;

QY 2 ATPASTPDTRALVADFGVYRLRQKGYVCGAGPGGPAADPLHQAYRAAGDESTRFRRTF 61
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Db 1 ATPASAPDTRALVEDFGVKLRQKGYVCGAGPGGPAADPLHQAYRAAGDESTRFRRTF 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 62 SDLAAQLHVTGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 121
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 SDLAAQLHVTGSAQQRFTQVSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQ 120
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QY 122 VQDMWVAYLETRLDWHSWGGAETALYGDGALEEARRLREGNWSVRTVLTGAVALG 181
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Db 121 VQDMWVAYLETRLDWHSWGGAETALYGDGALEEARRLREGNWSVRTVLTGAVALG 180
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QY 182 ALVTVGAFASK 193
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Db 181 ALVTVGAFASK 192
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RESULT 9
US-09-149-476-696
; Sequence 696, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; CURRENT FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
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; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,163
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/047,600
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,615
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,597
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,502
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,633
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,583
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,618
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,492
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,598
; EARLIER FILING DATE: 1997-05-23
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; EARLIER APPLICATION NUMBER: 60/047,582
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,596
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,612
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,632
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,601
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,580
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,671
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,674
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,669
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,312
; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
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; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/056,886
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,877
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,889
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,893
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,630
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,878
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,882
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; EARLIER APPLICATION NUMBER: 60/056,637
; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,888
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,879
; EARLIER FILING DATE: 1997-08-22
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EARLIER APPLICATION NUMBER: 60/056,880  
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EARLIER APPLICATION NUMBER: 60/056,911  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,636  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,874  
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EARLIER APPLICATION NUMBER: 60/056,910  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,864  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,631  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,845  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,892  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,761  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/047,595  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,599  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,588  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,585  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,586  
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EARLIER APPLICATION NUMBER: 60/047,590  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,594  
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EARLIER APPLICATION NUMBER: 60/047,589  
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EARLIER APPLICATION NUMBER: 60/047,593  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/047,614  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,578  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/043,576  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/047,501  
EARLIER FILING DATE: 1997-05-23  
EARLIER APPLICATION NUMBER: 60/043,670  
EARLIER FILING DATE: 1997-04-11  
EARLIER APPLICATION NUMBER: 60/056,632  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,664  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,876  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,881  
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EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,875  
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EARLIER APPLICATION NUMBER: 60/056,862  
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EARLIER APPLICATION NUMBER: 60/056,887  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/056,908  
EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/048,964  
EARLIER FILING DATE: 1997-06-06  
EARLIER APPLICATION NUMBER: 60/057,650  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/056,884

EARLIER FILING DATE: 1997-08-22  
EARLIER APPLICATION NUMBER: 60/057,669  
EARLIER FILING DATE: 1997-09-05  
EARLIER APPLICATION NUMBER: 60/049,610  
EARLIER FILING DATE: 1997-06-13  
EARLIER APPLICATION NUMBER: 60/061,060  
EARLIER FILING DATE: 1997-10-02  
Query Match 74.9%; Score 756; DB 4; Length 365;  
Best Local Similarity 97.9%; Pred. No. 8.9e-78;  
Matches 141; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFVGYKLRLQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALHVTGSAQQRFTQVSDDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALHVTGSAQQRFTQVSDDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMMVAYLETRLADWIHSSGGW 144  
DB 121 QVQEMMVAYLETRLADWIHSSGGW 144

RESULT 10  
US-09-271-014A-6  
Sequence 6, Application US/09271014A  
Patent No. 6395510  
GENERAL INFORMATION:  
APPLICANT: THOMPSON, CRAIG B.  
APPLICANT: BOISE, LAWRENCE H.  
TITLE OF INVENTION: VERTEBRATE APOPTOSIS GENE: COMPOSITIONS AND METHODS  
FILE REFERENCE: ARCD:316  
CURRENT APPLICATION NUMBER: US/09/271,014A  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 10  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 233  
TYPE: PRT  
ORGANISM: Human  
US-09-271-014A-6

Query Match 42.2%; Score 425.5; DB 4; Length 233;  
Best Local Similarity 40.6%; Pred. No. 2.1e-40;  
Matches 91; Conservative 24; Mismatches 58; Indels 51; Gaps 4;  
QY 11 RALVADFVGYRLRQKGYVC-----GAGP-----GEGPAA 39  
DB 6 RELVDFLSYKLSQGYSWQSQFSDVEENRTEAPEGTGSEMETPSAINGNPSWHLADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALHVTGSAQQRFTQ 81  
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSOLTSQLHITFGTAYQSFEQ 125  
QY 82 VSDELFOGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSS 141  
DB 126 VVNEIFRDGVMWGRIVAFVFGGALCVESVDKEMQVLVSRIAANMATYLNCHLEPWIQEN 185  
QY 142 GGWAFTALYGDGALEEARLRE--GNWASVKTVLTGAVALGAL 183  
DB 186 GGWDTFVELYGNNAAESRKQGERFNRFLTGMTVAGVLLGSL 229

RESULT 11  
US-08-333-565-59  
Sequence 59, Application US/08333565  
Patent No. 5622852  
GENERAL INFORMATION:  
APPLICANT: KORSMEYER, Stanley J.  
TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH  
TITLE OF INVENTION: REGULATOR

;/ NUMBER OF SEQUENCES: 59  
;/ CORRESPONDENCE ADDRESS:  
;/ ADDRESSEE: Townsend and Townsend Khourie and Crew  
;/ STREET: 379 Lytten Avenue  
;/ CITY: Palo Alto  
;/ STATE: California  
;/ COUNTRY: US  
;/ ZIP: 94301  
;/  
;/ COMPUTER READABLE FORM:  
;/ MEDIUM TYPE: Floppy disk  
;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/333,565  
;/ FILING DATE: 31-OCT-1994  
;/ CLASSIFICATION: 435  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: Smith, William M.  
;/ REGISTRATION NUMBER: 30,223  
;/ REFERENCE/DOCKET NUMBER: 15726A-000700  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: (415) 326-2400  
;/ TELEFAX: (415) 326-2422  
;/ INFORMATION FOR SEQ ID NO: 59:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 233 amino acids  
;/ TYPE: amino acid  
;/ STRANDEDNESS: single  
;/ TOPOLOGY: unknown  
;/ MOLECULE TYPE: peptide  
;/  
;/ US-08-333-565-59

Query Match 42.1%; Score 424.5; DB 1; Length 233;  
Best Local Similarity 40.9%; Pred. No. 2.7e-40;  
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYRLRKGY-----PLHQAMRAAGDBFETFRFRRTFSDLAALQHLHVTGSAQQRFT 80  
Db 6 RELVDFLSYKLSQKGSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGEPAAD-----PLHQAMRAAGDBFETFRFRRTFSDLAALQHLHVTGSAQQRFT 80  
Db 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDFELRYRRAFSDLTSQLHITPGTAYQSFE 124

QY 81 QVSDELFGGPNWGRIVAFVFFVFGAALCAESVKNKEMEPLVGQVQDMVAYLETRLADWIHS 140  
Db 125 QVWNELFROGVNWRIVAFVFFSFGGALCVESVDKEMQVLSRIAAMMATYLNHLEPWICE 184

QY 141 SGGWAEFTALYGDGALBEARLR--GNWASVTVLTGAVLALGAL 183  
Db 185 NGGWDTFVELYGNNAASRSKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 12  
US-08-081-448-6  
; Sequence 6, Application US/08081448  
; Patent No. 5646008  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Boise, Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; TITLE OF INVENTION: Compositions and Methods  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. 5646008th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

;/ COMPUTER: IBM PC compatible  
;/ OPERATING SYSTEM: PC-DOS/MS-DOS  
;/ SOFTWARE: PatentIn Release #1.0, Version #1.25  
;/ CURRENT APPLICATION DATA:  
;/ APPLICATION NUMBER: US/08/081,448  
;/ FILING DATE: 19930622  
;/ CLASSIFICATION: 424  
;/ ATTORNEY/AGENT INFORMATION:  
;/ NAME: No. 5646008thrup, Thomas E.  
;/ REGISTRATION NUMBER: 33,268  
;/ REFERENCE/DOCKET NUMBER: ARCD090  
;/ TELECOMMUNICATION INFORMATION:  
;/ TELEPHONE: 312-744-0090  
;/ TELEFAX: 312-755-4489  
;/ INFORMATION FOR SEQ ID NO: 6:  
;/ SEQUENCE CHARACTERISTICS:  
;/ LENGTH: 233 amino acids  
;/ TYPE: amino acid  
;/ TOPOLOGY: linear  
;/ MOLECULE TYPE: protein  
;/  
;/ US-08-081-448-6

Query Match 42.1%; Score 424.5; DB 1; Length 233;  
Best Local Similarity 40.2%; Pred. No. 2.7e-40;  
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYRLRKGY-----PLHQAMRAAGDBFETFRFRRTFSDLAALQHLHVTGSAQQRFTQ 81  
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QY 40 D-----PLHQAMRAAGDBFETFRFRRTFSDLAALQHLHVTGSAQQRFTQ 81  
Db 66 NGATAHSSSLDAREVIPMAAVKQALREAGDFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125

QY 82 VSDELFGGPNWGRIVAFVFFVFGAALCAESVKNKEMEPLVGQVQDMVAYLETRLADWIHSS 141  
Db 126 VVNELFROGVNWRIVAFVFFSFGGALCVESVDKEMQVLSRIAAMMATYLNHLEPWIQEN 185

QY 142 GGWAEFTALYGDGALBEARLR--GNWASVTVLTGAVLALGAL 183  
Db 186 GGWDTFVELYGNNAASRSKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 13  
US-08-607-269-24  
; Sequence 24, Application US/08607269  
; Patent No. 5702897  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; APPLICANT: Sato, Takaaki  
; TITLE OF INVENTION: Interaction of Proteins Involved in a  
; TITLE OF INVENTION: Cell Death Pathway  
; NUMBER OF SEQUENCES: 29  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell and Flores  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/607,269  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/226,876  
; FILING DATE: 13-APR-1994  
; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 9882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9032
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-607-269-24

Query Match 42.1%; Score 424.5; DB 1; Length 233;
Best Local Similarity 40.2%; Pred. No. 2.7e-40;
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYRLRQGY-----VCGAGP---GEGPAA 39
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QY 40 D-----PLHQAMRAAGDEFETFRFRRTFSDLAAQLHVTGSAQQRFTQ 81
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QY 82 VSDELFGGPNWGRIVAFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS 141
DB 126 VVNELFRDGVNWGRIVAFVFGGALCVESVDKEMQVLSRIAAMVATYLNHLEPWIQEN 185

QY 142 GGWAEFTALYGDGALBEARRLRE--GNWASVRTVLTGAVALGAL 183
DB 186 GGWDTFVELYGNNAABESRKQGERFNRWFLTGMTVAGVVLGSL 229

RESULT 14
US-08-471-058-14
; Sequence 14, Application US/08471058
; Patent No. 5770443
; GENERAL INFORMATION:
; APPLICANT: Kiefer, Michael C.
; APPLICANT: Barr, Philip J.
; TITLE OF INVENTION: NOVEL APOPTOSIS MODULATING
; TITLE OF INVENTION: PROTEINS, DNA ENCODING THE PROTEINS AND METHODS OF USE
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,058
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/320,157
; FILING DATE: 07-OCT-1994
; APPLICATION NUMBER: 08/160,067
; FILING DATE: 30-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 23647-20007.12
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792

; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-471-058-14

Query Match 42.1%; Score 424.5; DB 1; Length 233;
Best Local Similarity 40.9%; Pred. No. 2.7e-40;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

QY 11 RALVADFVGYRLRQGY-----V 28
DB 6 RELVDFLSYKLSQKGSWSQFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65

QY 29 CGAGPGECPAAD-----PLHQAMRAAGDEFETFRFRRTFSDLAAQLHVTGSAQQRFT 80
DB 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124

QY 81 QVSDELFGGPNWGRIVAFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHS 140
DB 125 QVVELFRDGVNWGRIVAFVFGGALCVESVDKEMQVLSRIAAMVATYLNHLEPWIQE 184

QY 141 SGWAEFTALYGDGALBEARRLRE--GNWASVRTVLTGAVALGAL 183
DB 185 NGWDTFVELYGNNAABESRKQGERFNRWFLTGMTVAGVVLGSL 229

RESULT 15
US-08-661-479-59
; Sequence 59, Application US/08661479
; Patent No. 5834209
; GENERAL INFORMATION:
; APPLICANT: KORSMEYER, Stanley J.
; TITLE OF INVENTION: Bcl-x/Bcl-2 ASSOCIATED CELL DEATH
; TITLE OF INVENTION: REGULATOR
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/661,479
; FILING DATE: 11-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,565
; FILING DATE: 31-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 15726A-000700
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 59:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-661-479-59

Query Match.	42.1%	Score 424.5;	DB 2;	Length 233;
Best local Similarity	40.9%	Pred. No. 2.7e-40;		
Matches	92;	Conservative 23;	Mismatches 57;	Indels 53; Gaps 4;

  

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QY	29	CGAGPGEGPAAD-----PLHQAMRAAGCDEFETRFRRTFSDLAAQLHVTTPGSAQQRF 90	
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DB	66	NGA-TGHSSSLDAREVPMNAVKQCALREAGDEFELRYRRAPFSDTSQLHITPGTAYQSPE 124	
QY	81	QVSDELFQGGPNWGRLVAFVFGAALCAESVNKEXEPLVGQVQDWMVAYLETRLADWIHS 140	
		:	
DB	125	QVNVNELFRDGVNWGRIVAFPSFGGALCVESVDKEMQVLVSRIAAMMATYLNLDHJEPWIQE 184	
QY	141	SGGWAEEFTALYGDGALSEARRLRE--GNWASVRTVLTGAVALGAL 183	
		:           :	
DB	185	NGGWDTFVELYGNNAAAESRKQERFNRRWFELTGMTVAGVVLGSL 229	

Search completed: October 24, 2003, 10:52:52  
Job time : 22 secs



GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: October 24, 2003, 10:51:15 ; Search time 45.5 Seconds  
(without alignments)  
710.328 Million cell updates/sec

Title: US-09-925-674A-9  
Perfect score: 1009  
Sequence: 1 MATPASTPDTRALVADFVGY.....JTGAVLGVTVGAFFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 3.5

Searched: 629382 seqs, 167460630 residues

Total number of hits satisfying chosen parameters: 629382

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*  
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18: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1009	100.0	193	10	US-09-925-674A-9 Sequence 9, Appli
2	997	98.8	193	10	US-09-925-674A-7 Sequence 7, Appli
3	756	74.9	365	11	US-09-809-391-696 Sequence 696, App
4	756	74.9	365	12	US-09-882-171-696 Sequence 696, App
5	424.5	42.1	233	9	US-09-734-846-2 Sequence 2, Appli
6	424.5	42.1	233	10	US-09-952-278-6 Sequence 6, Appli
7	424.5	42.1	233	12	US-10-169-223-10 Sequence 10, Appli
8	424.5	42.1	233	12	US-10-302-262-2 Sequence 2, Appli
9	424.5	42.1	233	15	US-10-101-482-14 Sequence 14, Appli
10	424.5	42.1	233	15	US-10-072-830-4 Sequence 4, Appli
11	411.5	40.8	152	15	US-10-158-769-2 Sequence 2, Appli
12	408.5	40.5	239	15	US-10-277-693A-10 Sequence 10, Appli
13	406.5	40.3	239	8	US-08-726-211-5 Sequence 5, Appli
14	406.5	40.3	239	12	US-10-141-618-12 Sequence 12, Appli
15	406.5	40.3	239	12	US-10-053-645A-21 Sequence 21, Appli

16	406.5	40.3	239	15	US-10-101-482-12	Sequence 12, Appli
17	406.5	40.3	239	15	US-10-072-830-2	Sequence 2, Appli
18	402	39.8	236	15	US-10-277-693A-11	Sequence 11, Appli
19	400	39.6	212	12	US-10-169-223-14	Sequence 14, Appli
20	375	37.2	190	10	US-09-952-278-2	Sequence 2, Appli
21	371.5	36.8	235	15	US-10-208-155-2	Sequence 2, Appli
22	370	36.7	155	15	US-10-158-769-1	Sequence 1, Appli
23	369.5	36.6	185	9	US-09-864-761-40954	Sequence 40954, A
24	342	33.9	205	8	US-08-726-211-7	Sequence 7, Appli
25	342	33.9	205	10	US-09-952-278-4	Sequence 4, Appli
26	342	33.9	205	12	US-10-053-645A-23	Sequence 23, Appli
27	241	23.9	49	9	US-09-864-761-34213	Sequence 34213, A
28	204	20.2	63	10	US-09-952-278-3	Sequence 3, Appli
29	180	17.8	170	10	US-09-952-278-8	Sequence 8, Appli
30	174	17.2	211	15	US-10-101-482-7	Sequence 7, Appli
31	174	17.2	211	15	US-10-101-482-10	Sequence 10, Appli
32	174	17.2	211	15	US-10-189-294-2	Sequence 2, Appli
33	174	17.2	211	15	US-10-177-293-25	Sequence 25, Appli
34	169	16.7	211	15	US-10-101-482-9	Sequence 9, Appli
35	169	16.7	211	15	US-10-101-482-11	Sequence 11, Appli
36	166.5	16.5	210	15	US-10-101-482-22	Sequence 22, Appli
37	156.5	15.5	192	15	US-10-277-693A-8	Sequence 8, Appli
38	154	15.3	191	15	US-10-196-793A-46	Sequence 46, Appli
39	154	15.3	192	12	US-10-306-878-5	Sequence 5, Appli
40	154	15.3	192	15	US-10-101-482-13	Sequence 13, Appli
41	154	15.3	192	15	US-10-277-693A-9	Sequence 9, Appli
42	154	15.3	280	15	US-10-101-482-19	Sequence 19, Appli
43	154	15.3	331	9	US-09-033-525-2	Sequence 2, Appli
44	153	15.2	192	15	US-10-277-693A-2	Sequence 2, Appli
45	153	15.2	212	12	US-10-299-514A-34	Sequence 34, Appli

ALIGNMENTS

RESULT 1

US-09-925-674A-9  
; Sequence 9, Application US/09925674A  
; Patent No. US20020119943A1  
; GENERAL INFORMATION:  
; APPLICANT: AMRAD Operations Pty Ltd  
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2  
; TITLE OF INVENTION: FAMILY OF APOPTOSIS-CONTROLLING GENES  
; FILE REFERENCE: 11686a  
; CURRENT APPLICATION NUMBER: US/09/925,674A  
; CURRENT FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: 09/925,674  
; PRIOR FILING DATE: 2001-08-09  
; PRIOR APPLICATION NUMBER: PN8965  
; PRIOR FILING DATE: 1996-03-27  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 193  
; TYPE: PRT  
; ORGANISM: Mouse  
US-09-925-674A-9

Query Match		100.0%;	Score 1009;	DB 10;	Length 193;
Best Local Similarity		100.0%;	Pred. No. 2e-101;		
Matches	193;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
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Dd	1	MATPASTPDTRALVADFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT	60		
QY	61	FSDLAAQLHVTGPSAQQRFTQVSDelfOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG	120		
Dd	61	FSDLAAQLHVTGPSAQQRFTQVSDelfOGGPNWGRLVAFVFGAALCAESVNKEMEPLVG	120		
QY	121	QVQDMVMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL	180		
Dd	121	QVQDMVMVAYLETRLDWIHSSGGWAEFTALYGDGALEEARRLREGNWSVRTVLTGAVAL	180		

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QY      181 GALVTVGAFPAK 193
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Db      181 GALVTVGAFPAK 193

RESULT 2
US-09-925-674A-7
; Sequence 7, Application US/09925674A
; Patent No. US20020119943A1
; GENERAL INFORMATION:
; APPLICANT: AMRAD Operations Pty Ltd
; TITLE OF INVENTION: A NOVEL MAMMALIAN GENE, bcl-w, BELONGS TO THE bcl-2
; FILE REFERENCE: 11686a
; CURRENT APPLICATION NUMBER: US/09/925,674A
; CURRENT FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/925,674
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: PN8965
; PRIOR FILING DATE: 1996-03-27
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 193
; TYPE: PRT
; ORGANISM: HUMAN
US-09-925-674A-7

Query Match      98.8%; Score 997; DB 10; Length 193;
Best Local Similarity 98.4%; Pred. NO. 4e-100;
Matches 190; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      61 FSDLAALQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120
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Db      61 FSDLAALQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120

QY      121 QVQDMVMVAYLETRLADWIHSSGGW 144
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Db      121 QVQDMVMVAYLETRLADWIHSSGGW 144

RESULT 4
US-09-892-171-696
; Sequence 696, Application US/09882171
; Publication No. US20030175858A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/882,171
; CURRENT FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 09/809,391
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 09/149,476
; PRIOR FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: PCT/US98/04493
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: 60/040,162
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,333
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/038,621
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/040,626
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; PRIOR FILING DATE: 1997-03-07
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; PRIOR APPLICATION NUMBER: 60/040,163
; PRIOR FILING DATE: 1997-03-07
; PRIOR APPLICATION NUMBER: 60/047,600
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,615
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,597
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,502
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,633
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,583
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,617
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,618
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,503
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,592
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,581
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,584
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,500
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,587
; PRIOR FILING DATE: 1997-05-23
; PRIOR APPLICATION NUMBER: 60/047,492
; PRIOR FILING DATE: 1997-05-23

QY      1 MATPASTPDTRALVADFVGYYRLRQKGYVCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60
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Db      1 MATPASAPDTRALVADFVGYYKLRLQKGYVCGAGPGGPAADPLHQAAMRAAGDEFETRFRRT 60

QY      61 FSDLAALQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120
      |||||
Db      61 FSDLAALQLHVTTPGSAQQRFTQVSDQLFQGGPNWGRLLVAFFVFGAALCAESVNKEMEPLVG 120

QY      121 QVQDMVMVAYLETRLADWIHSSGGW 144
      |||||
Db      121 QVQDMVMVAYLETRLADWIHSSGGW 144

Query Match      74.9%; Score 756; DB 11; Length 365;
Best Local Similarity 97.9%; Pred. NO. 1.4e-73;
Matches 141; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      181 GALVTVGAFPAK 193
      |||||
Db      181 GALVTVGAFPAK 193

RESULT 3
US-09-809-391-696
; Sequence 696, Application US/09809391
; Publication No. US20030049618A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 186 Human Secreted proteins
; FILE REFERENCE: PZ002P2
; CURRENT APPLICATION NUMBER: US/09/809,391
; CURRENT FILING DATE: 2001-03-16
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 761
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 696
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-809-391-696
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; PRIOR APPLICATION NUMBER: 60/047,598  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,613  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,582  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,596  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,612  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,632  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/047,601  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,580  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,568  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,314  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,569  
; PRIOR FILING DATE: 1997-04-11  
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; PRIOR FILING DATE: 1997-04-11  
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; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/056,886  
; PRIOR FILING DATE: 1997-08-22  
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; PRIOR FILING DATE: 1997-08-22  
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; PRIOR FILING DATE: 1997-08-22  
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; PRIOR APPLICATION NUMBER: 60/056,880  
; PRIOR FILING DATE: 1997-08-22  
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; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,636

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; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,874  
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; PRIOR APPLICATION NUMBER: 60/056,910  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,864  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,631  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,845  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,892  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,761  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/047,595  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
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; PRIOR APPLICATION NUMBER: 60/047,589  
; PRIOR FILING DATE: 1997-05-23  
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; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,578  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/043,576  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/047,501  
; PRIOR FILING DATE: 1997-05-23  
; PRIOR APPLICATION NUMBER: 60/043,670  
; PRIOR FILING DATE: 1997-04-11  
; PRIOR APPLICATION NUMBER: 60/056,632  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,664  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,876  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,881  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,909  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,875  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,862  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,887  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/056,908  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/048,964  
; PRIOR FILING DATE: 1997-06-06  
; PRIOR APPLICATION NUMBER: 60/057,650  
; PRIOR FILING DATE: 1997-09-05  
; PRIOR APPLICATION NUMBER: 60/056,884  
; PRIOR FILING DATE: 1997-08-22  
; PRIOR APPLICATION NUMBER: 60/057,669  
; PRIOR FILING DATE: 1997-09-05

Query Match 74.9%; Score 756; DB 12; Length 365;  
Best Local Similarity 97.9%; Pred. No. 1.4e-73;  
Matches 141; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATPASTPDTRALVADFVGYYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
DB 1 MATPASAPDTRALVADFVGYYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
QY 61 FSDLAALQHLVTPGSAQQRFTQVSDVDFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
DB 61 FSDLAALQHLVTPGSAQQRFTQVSDVDFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
QY 121 QVQDMVMVAYLETRLADWIHSSGGW 144  
DB 121 QVQDMVMVAYLETRLADWIHSSGGW 144

RESULT 5

US-09-734-846-2  
; Sequence 2, Application US/09734846  
; Patent No. US20010007025A1  
; GENERAL INFORMATION:  
; APPLICANT: Bennett, C. Frank  
; APPLICANT: Dean, Nicholas M.  
; APPLICANT: Monia, Brett P.  
; APPLICANT: Nickoloff, Brian J.  
; APPLICANT: Zhang, Qingqing  
; TITLE OF INVENTION: Antisense Modulation of bcl-x Expression  
; FILE REFERENCE: ISPH-0528  
; CURRENT APPLICATION NUMBER: US/09/734,846  
; CURRENT FILING DATE: 2000-12-12  
; PRIOR APPLICATION NUMBER: 09/277,020  
; PRIOR FILING DATE: 1998-03-26  
; PRIOR APPLICATION NUMBER: 09/167,921  
; PRIOR FILING DATE: 1998-10-07  
; PRIOR APPLICATION NUMBER: 09/323,743  
; PRIOR FILING DATE: 1999-06-02  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-734-846-2

Query Match 42.1%; Score 424.5; DB 9; Length 233;  
Best Local Similarity 40.2%; Pred. No. 7.5e-38;  
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYYRLRQKGY-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRFTQ 39  
DB 6 RELVDFLSYKLSQKGYSNQSFSDVEENRTEAPEGTESEMETPTSAINGNPSWHLADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRFTQ 81  
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125  
QY 82 VSDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDMVMVAYLETRLADWIHSS 141  
DB 126 VVNELFRDGVNWGRIVAFVFGGALCVESVDKEMQVLSRIAAMNATYLNNDHLEPWIQEN 185  
QY 142 GGWAEFTALYGDGALAEARRLRE--GNWASVRTVLTGAVALLGAL 183  
DB 186 GGWDTFVELYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 6

US-09-952-278-6  
; Sequence 6, Application US/09952278  
; Patent No. US20020137182A1  
; GENERAL INFORMATION:  
; APPLICANT: Thompson, Craig B.  
; APPLICANT: Boise, Lawrence H.  
; TITLE OF INVENTION: Vertebrate Apoptosis Gene:  
; Compositions and Methods  
; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: 321 No. US20020137182A1th Clark Street, Suite 800  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60610  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/952,278  
; FILING DATE: 12-Sep-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/081,448  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: No. US20020137182A1thrup, Thomas E.  
; REGISTRATION NUMBER: 33,268  
; REFERENCE/DOCKET NUMBER: ARCD090  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-744-0090  
; TELEFAX: 312-755-4489  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 233 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-09-952-278-6

Query Match 42.1%; Score 424.5; DB 10; Length 233;  
Best Local Similarity 40.2%; Pred. No. 7.5e-38;  
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;

QY 11 RALVADFVGYYRLRQKGY-----VCGAGP-----GEGPAA 39  
DB 6 RELVDFLSYKLSQKGYSNQSFSDVEENRTEAPEGTESEMETPTSAINGNPSWHLADSPAV 65  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRFTQ 81  
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125  
QY 82 VSDELFGQGNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDMVMVAYLETRLADWIHSS 141  
DB 126 VVNELFRDGVNWGRIVAFVFGGALCVESVDKEMQVLSRIAAMNATYLNNDHLEPWIQEN 185  
QY 142 GGWAEFTALYGDGALAEARRLRE--GNWASVRTVLTGAVALLGAL 183  
DB 186 GGWDTFVELYGNNAEAESRKQGERFNRWFLTGMTVAGVLLGSL 229

RESULT 7

US-10-169-223-10  
; Sequence 10, Application US/10169223  
; Publication No. US20030152946A1  
; GENERAL INFORMATION:  
; APPLICANT: SHIMIZU, Shigeomi  
; APPLICANT: TSUJIMOTO, Yoshihide  
; TITLE OF INVENTION: BH4-Fused Polypeptides  
; FILE REFERENCE: 1422-0537P  
; CURRENT APPLICATION NUMBER: US/10/169,223  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: JP 11-371449  
; PRIOR FILING DATE: 1999-12-27  
; PRIOR APPLICATION NUMBER: PCT/JP00/09274  
; PRIOR FILING DATE: 2000-12-26  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: PatentIn version 3.1





US-10-072-830-4  
; Sequence 4, Application US/10072830  
; Publication No. US20030103945A1  
; GENERAL INFORMATION:  
; APPLICANT: CHEN, DONG FENG  
; APPLICANT: HUANG, XIZHONG  
; APPLICANT: CHEN, GUANG  
; APPLICANT: MANJI, HUSSEINI K.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR STIMULATING AXON  
; TITLE OF INVENTION: REGENERATION AND PREVENTING NEURONAL CELL DEGENERATION  
; FILE REFERENCE: ERM-105.01  
; CURRENT APPLICATION NUMBER: US/10/072,830  
; CURRENT FILING DATE: 2002-02-08  
; PRIOR APPLICATION NUMBER: 60/267,832  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: 60/272,617  
; PRIOR FILING DATE: 2001-03-01  
; PRIOR APPLICATION NUMBER: 60/289,990  
; PRIOR FILING DATE: 2001-05-10  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 233  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-072-830-4  
  
Query Match 42.1%; Score 424.5; DB 15; Length 233;  
Best Local Similarity 40.2%; Pred. No. 7.5e-38;  
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;  
  
QY 11 RALVADFVGYRLRQKGY-----VCGAGP-----GEGPAA 39  
DB 6 RELVWDFLSYKLSQKGSWSQFSDEVENRTEAPEGTESEYETPSAINGNPSWHLADSPAV 65  
  
QY 40 D-----PLHQAMRAAGDEFETRFRRTFSDLAALQLHVTGPSAQQRFTQ 81  
DB 66 NGATAHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSEFQ 125  
  
QY 82 VSDELFGQGNWGLVAFVFGAALCAESVKNKMEPLVGQVQDMVAYLETRLADWIHSS 141  
DB 126 VVNELFRDGVNWRGRIVAFVFGGALCVESVDKEMQVLVSRIAAWMATYLNHLEPWIQEN 185  
  
QY 142 GGWAEFTALYDGALEEARLRE--GNWASVRTVLTGAVALGAL 183  
DB 186 GGWDTFVELYGNNAAESRKQERFNRWFLTGMTVAGVVJGSL 229  
  
RESULT 11  
US-10-158-769-2  
; Sequence 2, Application US/10158769  
; Publication No. US20030008924A1  
; GENERAL INFORMATION:  
; APPLICANT: Weng, Shaomeng  
; APPLICANT: Yang, Dajun  
; TITLE OF INVENTION: Small Molecule Antagonists of Bcl-2 Family Protein  
; FILE REFERENCE: UM-07232  
; CURRENT APPLICATION NUMBER: US/10/158,769  
; CURRENT FILING DATE: 2002-09-09  
; PRIOR APPLICATION NUMBER: 60/293,983  
; PRIOR FILING DATE: 2001-05-30  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 152  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-158-769-2  
  
Query Match 40.8%; Score 411.5; DB 15; Length 152;  
Best Local Similarity 52.3%; Pred. No. 1.1e-36;

Matches 79; Conservative 18; Mismatches 45; Indels 9; Gaps 1;  
  
QY 11 RALVADFVGYRLRQKGYCG-----AGPEGPAADPLHQAMRAAGDEFETRFRRTF 61  
DB 2 RELVWDFLSYKLSQKGSWSQFSDEVENRTEAPEGTESEAVKQALREAGDEFELRYRRAF 61  
  
QY 62 SDLAAQLHVTGPSAQQRFTQVSDELFGQGNWGLVAFVFGAALCAESVKNKMEPLVGQ 121  
DB 62 SDLTSQLHITPGTAYQSFQVNVNELFRDGVNWRGRIVAFVFGGALCVESVDKEMQVLVSR 121  
  
QY 122 VQDMVAYLETRLADWIHSSGGWAEFTALYG 152  
DB 122 IAAWMATYLNHLEPWIQENGGWDTFVELYG 152  
  
RESULT 12  
US-10-277-693A-10  
; Sequence 10, Application US/10277693A  
; Publication No. US20030096367A1  
; GENERAL INFORMATION:  
; APPLICANT: Korsmeyer, Stanley J.  
; TITLE OF INVENTION: Cell Death Agonists  
; FILE REFERENCE: 56029/36280  
; CURRENT APPLICATION NUMBER: US/10/277,693A  
; CURRENT FILING DATE: 2002-10-22  
; PRIOR APPLICATION NUMBER: 09/379,820  
; PRIOR FILING DATE: 1999-08-24  
; PRIOR APPLICATION NUMBER: 08/112,208  
; PRIOR FILING DATE: 1993-08-26  
; PRIOR APPLICATION NUMBER: 08/856,034  
; PRIOR FILING DATE: 1997-05-14  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-277-693A-10  
  
Query Match 40.5%; Score 408.5; DB 15; Length 239;  
Best Local Similarity 36.6%; Pred. No. 4.2e-36;  
Matches 86; Conservative 35; Mismatches 59; Indels 55; Gaps 5;  
  
QY 9 DTRALVADFVGYRLRQKGYVCGAG-----PGE----- 35  
DB 10 DNREIVMKYIHYKLSQKGSWSQFSDEVENRTEAPEGTESEAVKQALREAGDEFELRYRRAF 69  
  
QY 36 -----GPAADP-----LHQAMRAAGDEFETRFRRTFSDLAALQLHVTGPSAQQR 78  
DB 70 SPLQTPAAPGAAAGPALSPPVPPVHLLTRAGDDFSRRYRRDFAEMSSQLHLTPFTTARGR 129  
  
QY 79 FTQVSDELFGQGNWGLVAFVFGAALCAESVKNKMEPLVGQVQDMVAYLETRLADWI 138  
DB 130 FATWVEELFRDGVNWRGRIVAFVFGGALCVESVKNREMSPLVDNIALMWTEYLNRLHTWI 189  
  
QY 139 HSSGGWAEFTALYDGALEEARLREGNWNASVRTVLTGAVALGALVTGAPFASK 193  
DB 190 QDNGGWDADFVELYG----PSMRPLDFDSWLSLKLTLAL-VGACITLGAYLGHK 239  
  
RESULT 13  
US-08-726-211-5  
; Sequence 5, Application US/08726211  
; Publication No. US20030012812A1  
; GENERAL INFORMATION:  
; APPLICANT: Tormo, Mar  
; APPLICANT: Tari, Ana M.  
; APPLICANT: Lopez-Berestein, Gabriel  
; TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
; TITLE OF INVENTION: LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES  
; NUMBER OF SEQUENCES: 7  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/726,211  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Wilson, Mark B.  
REGISTRATION NUMBER: 37,259  
REFERENCE/DOCKET NUMBER: JTXC:504  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-726-211-5

Query Match 40.3%; Score 406.5; DB 8; Length 239;  
Best Local Similarity 36.6%; Pred. No. 7e-36;  
Matches 86; Conservative 36; Mismatches 58; Indels 55; Gaps 5;  
QY 9 DTRALVADFVG YRLRQKGYVCGAG-----PGE----- 35  
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Db 10 DNREIVMKYIHYKLSQRGYEWDAAGVGAAPGAPGIFSSQPGHTPHPAASRDVPART 69  
QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAALHVTTPGSAQQR 78  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 70 SPLQTPAAPGAAAGPALSPPVPPVHLLALRQAGDDFSRRYRGDFAEEMSSQLHLTPFTARGR 129  
QY 79 FTQVSDLELFOGGPNWGRILVAFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138  
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QY 139 HSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALGALVTVGAFFASK 193  
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Db 190 QDNGGWDAFVELYG----PSMRPLDFDSWLSLKTLLSLAL-VGACITLGAYLSHK 239

RESULT 14  
US-10-141-618-12  
; Sequence 12, Application US/10141618  
; Publication No. US20030165887A1  
; GENERAL INFORMATION:  
; APPLICANT: Reed, John C.  
; TITLE OF INVENTION: Methods For Determining the Prognosis  
; FILE REFERENCE: P-LJ 5254  
; CURRENT APPLICATION NUMBER: US/10/141,618  
; CURRENT FILING DATE: 2002-05-07  
; PRIOR APPLICATION NUMBER: US 60/289,233  
; PRIOR FILING DATE: 2001-05-07  
; PRIOR APPLICATION NUMBER: US 60/356,934  
; PRIOR FILING DATE: 2002-02-12  
; PRIOR APPLICATION NUMBER: US 09/388,221  
; PRIOR FILING DATE: 1999-09-01  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: Fastseq for Windows Version 4.0  
; SEQ ID NO 12  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo sapiens

US-10-141-618-12  
Query Match 40.3%; Score 406.5; DB 12; Length 239;  
Best Local Similarity 36.6%; Pred. No. 7e-36;  
Matches 86; Conservative 36; Mismatches 58; Indels 55; Gaps 5;  
QY 9 DTRALVADFVG YRLRQKGYVCGAG-----PGE----- 35  
| | | | | : : : : : | | | | |  
Db 10 DNREIVMKYIHYKLSQRGYEWDAAGVGAAPGAPGIFSSQPGHTPHPAASRDVPART 69  
QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAALHVTTPGSAQQR 78  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 70 SPLQTPAAPGAAAGPALSPPVPPVHLLALRQAGDDFSRRYRGDFAEEMSSQLHLTPFTARGR 129  
QY 79 FTQVSDLELFOGGPNWGRILVAFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 130 FATVVEELFRDGVNMGRIVAFVFGGVMCVESVNREMSPLVDNIALWMTTEYLNRHLHTWI 189  
QY 139 HSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALGALVTVGAFFASK 193  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 190 QDNGGWDAFVELYG----PSMRPLDFDSWLSLKTLLSLAL-VGACITLGAYLSHK 239

RESULT 15  
US-10-053-645A-21  
; Sequence 21, Application US/10053645A  
; Publication No. US20030176376A1  
; GENERAL INFORMATION:  
; APPLICANT: Robert E. Klem  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING A  
; TITLE OF INVENTION: CELL-PROLIFERATIVE DISORDER USING CRE DECOY OLIGOMERS, BCL-2  
; TITLE OF INVENTION: ANTISENSE OLIGOMERS, AND HYBRID OLIGOMERS THEREOF  
; FILE REFERENCE: 10412-022-999  
; CURRENT APPLICATION NUMBER: US/10/053,645A  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/263,244  
; PRIOR FILING DATE: 2001-01-22  
; NUMBER OF SEQ ID NOS: 43  
; SOFTWARE: Fastseq for Windows Version 4.0  
; SEQ ID NO 21  
; LENGTH: 239  
; TYPE: PRT  
; ORGANISM: Homo Sapiens  
US-10-053-645A-21

Query Match 40.3%; Score 406.5; DB 12; Length 239;  
Best Local Similarity 36.6%; Pred. No. 7e-36;  
Matches 86; Conservative 36; Mismatches 58; Indels 55; Gaps 5;  
QY 9 DTRALVADFVG YRLRQKGYVCGAG-----PGE----- 35  
| | | | | : : : : : | | | | |  
Db 10 DNREIVMKYIHYKLSQRGYEWDAAGVGAAPGAPGIFSSQPGHTPHPAASRDVPART 69  
QY 36 -----GPAADP-----LHQAMRAAGDEFETFRFRRTFSDLAALHVTTPGSAQQR 78  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 70 SPLQTPAAPGAAAGPALSPPVPPVHLLALRQAGDDFSRRYRGDFAEEMSSQLHLTPFTARGR 129  
QY 79 FTQVSDLELFOGGPNWGRILVAFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWI 138  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 130 FATVVEELFRDGVNMGRIVAFVFGGVMCVESVNREMSPLVDNIALWMTTEYLNRHLHTWI 189  
QY 139 HSSGGWAEFTALYGDGALEEARRLREGNWNASVRTVLTGAVALGALVTVGAFFASK 193  
| | | | | : : : : : | | | | | : : : : : | | | | |  
Db 190 QDNGGWDAFVELYG----PSMRPLDFDSWLSLKTLLSLAL-VGACITLGAYLSHK 239

Search completed: October 24, 2003, 11:04:41  
Job time : 46.5 secs

GenCore version 5.1.6  
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CM protein - protein search, using sw model

Run on: October 24, 2003, 10:44:00 ; Search time 25 Seconds  
(without alignments)  
742.422 Million cell updates/sec

Title: US-09-925-674A-9  
Perfect score: 1009  
Sequence: 1 MATPASTPDTRALVADFVG.....LTGAVAGALVTVGAFPAASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	425.5	42.2	233	2 I49056	bcl-x long - mouse
2	424.5	42.1	233	2 B47537	apoptosis regulato
3	421.5	41.8	233	2 S51761	BCL-X protein - ra
4	420.5	41.7	233	2 A37332	transforming prote
5	411	40.7	232	2 S24390	transforming prote
6	408.5	40.5	239	1 TVHUA1	transforming prote
7	408	40.4	236	2 I67432	BCL-2 - rat fragm
8	403	39.9	236	2 I53744	gene bcl-2 protein
9	402	39.8	236	1 TVMSA1	transforming prote
10	401.5	39.8	233	2 I67431	BCL-X-long - rat
11	399	39.5	236	2 JC7383	B-cell lymphoma 2
12	375	37.2	190	2 A47537	apoptosis regulato
13	374.5	37.1	214	2 I49057	bcl-x transmembran
14	371.5	36.8	227	2 JE0203	apoptosis regulato
15	353	35.0	216	2 B37332	transforming prote
16	345.5	34.2	199	1 TVMSB1	transforming prote
17	342	33.9	205	1 TVHUB1	transforming prote
18	277.5	27.5	154	2 I58194	gene bcl-2 protein
19	179	17.7	170	2 I49055	bcl-x short - mous
20	174	17.2	211	2 S58873	Bak protein - huma
21	171	16.9	176	2 I67435	gene bcl-xshort pr
22	169	16.7	211	2 S58875	cdh-2 protein - hu
23	158.5	15.7	192	2 D47538	bcl-2-associated p
24	154	15.3	192	2 A47538	bcl-2-associated p
25	154	15.3	261	2 H68578	protein ced-9 limp
26	154	15.3	280	2 A53189	apoptosis suppress
27	150.5	14.9	133	2 I53295	bcl-2-associated p
28	147.5	14.6	179	2 JC7255	Bax-delta protein
29	147.5	14.6	218	2 B47538	bcl-2-associated p

30	144	14.3	177	2 S54778	NR-13 protein - qu
31	141	14.0	255	2 JC7567	Mcl-1a protein - z
32	138.5	13.7	143	2 I38921	bcl-2-associated p
33	119	11.8	175	2 I39055	Bcl-2 related - hu
34	116	11.5	350	2 A47476	BCL2 homolog MCL1
35	105	10.4	172	2 I49449	hemopoietic-specif
36	88	8.7	185	2 B83217	hypothetical prote
37	86.5	8.6	301	2 T36534	probable lipase/es
38	86.5	8.6	3433	1 GNWVKV	genome polyprotein
39	86	8.5	270	2 A12598	dihydrodipicolinat
40	86	8.5	279	2 B97381	glutamate-ammonia
41	83.5	8.3	358	1 AJLCQB	alanine-tRNA ligas
42	83.5	8.3	872	2 G98026	alanine-tRNA synthe
43	83.5	8.3	872	2 H95160	genome polyprotein
44	82.5	8.2	3430	1 GNWVWV	beta-amyloid-like
45	81.5	8.1	886	2 A32758	

ALIGNMENTS

RESULT 1  
I49056  
bcl-x long - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 16-Jul-1999  
C;Accession: I49056; S52866  
R;Fang, W.; Rivard, J.J.; Mueller, D.L.; Behrens, T.W.  
J. Immunol. 153, 4388-4398, 1994  
A;Title: Cloning and molecular characterization of mouse bcl-x in B and T lymphocytes.  
A;Reference number: I49055; MUID:95052604; PMID:7963517  
A;Accession: I49056  
A;Status: preliminary; translated from GB/EMBL/DCDBJ  
A;Molecule type: mRNA  
A;Residues: 1-233 <RES>  
A;Cross-references: EMBL:U10101; NID:G506647; PIDN:AAA82173.1; PID:G506648  
R;Kamesaki, H.; Michaud, G.Y.; Takatsu, K.; Okuma, M.  
submitted to the EMBL Data Library, November 1994  
A;Description: IL-5 inhibits anti-IgM-induced apoptosis in an immature B cell line thr  
A;Reference number: S52866  
A;Accession: S52866  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-233 <KAM>  
A;Cross-references: EMBL:X83574; NID:G695622; PIDN:CAA58557.1; PID:G695623  
C;Superfamily: bcl transforming protein

Query Match 42.2%; Score 425.5; DB 2; Length 233;  
Best Local Similarity 40.9%; Pred. No. 4.2e-32;  
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

Qy	11	RALVADFVGRLRQKGY-----V 28
Db	6	RELVDFLSYKLSQKGSWSQFSDFVEENRTEAPEETEARETPSAINGNPSWHLADSPAV 65
Qy	29	CGAGPGEGPAAD-----PLHQAMRAAGDEFETRFRRTTFSDLAQLHVTTPGSAQQRFT 80
Db	66	NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
Qy	81	QVSDELFQGGPNWGRLVAFVFGAALCAESVNMKEMEPLVGQVQDMVMVAYLETRLADWIHS 140
Db	125	QVWNELFRDGWNWGRIVAFVFFSGGALCVESVDKEMQVLVSRIASWMATYLNHLEPWIQE 184
Qy	141	SGGWAEEFTALYGGGALJEEARRLRE--GNWASVRTVLTVGAVAGAL 183
Db	185	NGGWDTFVDLYGNNAAESRKQERFNRFLTGMTVAGVVLGSL 229

RESULT 2  
B47537  
apoptosis regulator bcl-xL - human  
N;Alternate names: bcl-2-related protein  
N;Contains: apoptosis regulator bcl-xs







```

RESULT 8
I53744
gene bcl-2 protein - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 16-Jul-1999
C;Accession: I53744
R;Sato, T.; Irie, S.; Krajewski, S.; Reed, J.C.
Gene 140, 291-292, 1994
A;Title: Cloning and sequencing of a cDNA encoding the rat Bcl-2 protein.
A;Reference number: I53744; MUID:94193015; PMID:814404
A;Accession: I53744
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-236 <RES>
A;Cross-references: GB:L14680; NID:g408946; PIDN:AAA53662.1; PID:g408947
C;Genetics:
A;Gene: bcl-2
C;Superfamily: bcl transforming protein

Query Match 39.9%; Score 403; DB 2; Length 236;
Best Local Similarity 35.3%; Pred. No. 5.2e-30;
Matches 82; Conservative 35; Mismatches 63; Indels 52; Gaps 3;

QY 9 DTRALVADFVGRLRQKGY----- 27
D 10 DNREIVMKYIHYKLSQRGYEWDTGDEDSAPLRAAPTGGIFSFQPSNTPAVHRDTAART 69
QY 28 -----VCGAGPGEGPADPLHQAMRAAGDEPETFRRTFSDLAALHVTGSAQQRFQ 81
D 70 SPLRPLVANAGPALSPVPPVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
QY 82 VSDELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSS 141
D 130 VVEELFRDGVNWGRIVAFVFGVGMVGVSVNREMSPLVDNIAJMWTEYLNRRHLHTWIQDN 189
QY 142 GGWAEFTALYGDGALEEARLRREGNWNASVRTVLTGAVALGALVTVGAFFASK 193
D 190 GGWDAFVELYG----PSMRPLDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236

RESULT 9
TVMSA1
transforming protein bcl-2-alpha - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Jun-1999
C;Accession: A25960; E37332
R;Negrini, M.; Silini, E.; Kozak, C.; Tsujimoto, Y.; Croce, C.M.
Cell 49, 455-463, 1987
A;Title: Molecular analysis of mbcl-2: structure and expression of the murine gene homolog
A;Reference number: A90893; MUID:87167643; PMID:3032455
A;Accession: A25960
A;Molecule type: DNA
A;Residues: 1-236 <NEG>
A;Cross-references: GB:L31532; GB:M16506; NID:g468336; PIDN:AAA37282.1; PID:g387109
R;Eguchi, Y.; Ewert, D.L.; Tsujimoto, Y.
Nucleic Acids Res. 20, 4187-4192, 1992
A;Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety
A;Reference number: A37332; MUID:92375724; PMID:1508712
A;Accession: E37332
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 1-33, 'E', 34-220, 'AL', 223-236 <EGU>
C;Genetics:
A;Gene: BCL2
A;Introns: 192/3
C;Superfamily: bcl transforming protein
C;Keywords: alternative splicing; mitochondrion; transforming protein; transmembrane pro

Query Match 39.8%; Score 402; DB 1; Length 236;
Best Local Similarity 36.6%; Pred. No. 6.5e-30;
Matches 85; Conservative 34; Mismatches 61; Indels 52; Gaps 5;

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```

QY 9 DTRALVADFVGRLRQKGYCGAG-----PG----- 34
D 10 DNREIVMKYIHYKLSQRGYEWDAADAAPLGAAPTGGIFSFQPSNTPAVHREYAART 69
QY 35 -----EGPAADP-----LHQAMRAAGDEPETFRRTFSDLAALHVTGSAQQRFQ 81
D 70 SPLRPLVATAGPALSPVPPCVHLTLRRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
QY 82 VSDELFGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHSS 141
D 130 VVEELFRDGVNWGRIVAFVFGVGMVGVSVNREMSPLVDNIAJMWTEYLNRRHLHTWIQDN 189
QY 142 GGWAEFTALYGDGALEEARLRREGNWNASVRTVLTGAVALGALVTVGAFFASK 193
D 190 GGWDAFVELYG----PSMRPLDFSWLSLKTLLS-LPWVGACITLGAYLGHK 236

RESULT 10
I67431
BCL-X-Jong - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C;Accession: I67431
R;Tilly, J.L.; Tilly, K.I.; Kenton, M.L.; Johnson, A.L.
Endocrinology 136, 232-241, 1995
A;Title: Expression of members of the bcl-2 gene family in the immature rat ovary: equ
onstitutive bcl-2 and bcl-xlong messenger ribonucleic acid levels.
A;Reference number: I53295; MUID:95129487; PMID:7828536
A;Accession: I67431
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-233 <RES>
A;Cross-references: EMBL:U34963; NID:gi004376; PIDN:AAA77686.1; PID:gi004377
C;Superfamily: bcl transforming protein

Query Match 39.8%; Score 401.5; DB 2; Length 233;
Best Local Similarity 39.1%; Pred. No. 7.1e-30;
Matches 88; Conservative 23; Mismatches 61; Indels 53; Gaps 4;

QY 11 RALVADFVGRLRQKGY-----V 28
D 6 RELVDFLSYKLSQKGSWSQSFSDVEENRTEAPEETEPEPETPSAINGNPSWHLADSPAV 65
QY 29 CGAGPGEGPAD-----PLHQAMRAAGDEPETFRRTFSDLAALHVTGSAQQRFQ 80
D 66 NGA-TGHSSSLDAREVLPMAAVKQALREAGDEFELRYRRAFSDLSQLHITPGTVYQSFE 124
QY 81 QVSDELFQGGPNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHS 140
D 125 QVVNELFRDGVNWGRIVASSSFGGALCVESVDKEMQVLSVRIASWMTATYLNHLEPWIOE 184
QY 141 SGGWAEFTALYGDGALEEARLRRE--GNWASVRTVLTGAVALGAL 183
D 185 NGGWDTFVDLYGNNTAPESRKQGERFNRWFLTGMTVAGVVLGSL 229

RESULT 11
JC7383
B-cell lymphoma 2 protein - Chinese hamster
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 08-Dec-2000
C;Accession: JC7383
R;Tomicić, M.T.; Christmann, M.; Kaina, B.
Biochem. Biophys. Res. Commun. 275, 899-903, 2000
A;Title: Cloning and functional analysis of cDNA encoding the hamster Bcl-2 protein.
A;Reference number: JC7383
A;Contents: Ovary
A;Accession: JC7383
A;Molecule type: mRNA
A;Residues: 1-236 <TOM>
A;Cross-references: GB:AJ271720
C;Comment: This protein has anti-apoptotic function, and supports cell survival.
C;Genetics:

```





transforming protein (bcl-2-beta) - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 24-Apr-1998  
C:Accession: B37332; S35452  
R:Eguchi, Y.; Ewert, D.J.; Tsujimoto, Y.  
Nucleic Acids Res. 20, 4187-4192, 1992  
A:Title: Isolation and characterization of the chicken bcl-2 gene: expression in a variety of tissues  
A:Reference number: A37332; MUID:92375724; PMID:1508712  
A:Accession: B37332  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 1-216 <EGU>  
A:Cross-references: EMBL:D11381; EMBL:D11382  
C:Superfamily: bcl transforming protein

Query Match	35.0%;	Score 353;	DB 2;	Length 216;	
Best Local Similarity	37.8%;	Pred. No. 2.1e-25;			
Matches	70;	Conservative	22;	Mismatches 49;	
			Indels	44;	
			Gaps	2;	
QY	9	DTRALVADFVG	YRLRQKGYVCGAG	-----PGECPAADP-----41	
DB	10	DNREIVLKYI	HYKLSQRGYDWAAGEDRPPVP	PAPAPAPAAAPAAVAAGASSHHRPEPPGSA69	
QY	42	-----	-----LHQAMRAAGDE	FETFRRTFSDLAAQLHVT	PGSAQQRFTQVSD84
DB	70	AASEVPPAEG	LRPAPPGVHLALRQAGDE	FSRRYQRDFAQMSGQLHLTP	FTAHGRFVAVVE129
QY	85	ELFQGGPNW	GRLVAFVFGAALCAESV	NKMEPLVGVQVQDMMVAY	LETRLADWIHSSGGW144
DB	130	ELFRDGVNW	GRIVAFPEFGVMCMVES	VNREMSPLVDNIATMTTEYL	NRHLHNWIQDNGGW189
QY	145	AEFTA	149		
DB	190	VRACA	194		

Search completed: October 24, 2003, 10:52:03  
Job time : 26 secs

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OMPprotein - protein search, using sw model

Run on: October 24, 2003, 10:26:35 ; Search time 13.5 Seconds  
(without alignments)  
672.308 Million cell updates/sec

Title: US-09-925-674A-9  
Perfect score: 1009  
Sequence: 1 MATPASTPTDTRALVADFGY.....LTGAVALGALVTVGAPFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1006	99.7	193	1 BCLW_MOUSE	P70345 mus musculus
2	997	98.8	193	1 BCLW_HUMAN	Q92843 homo sapien
3	647.5	64.2	228	1 AR1_XENLA	Q91827 xenopus lae
4	429.5	42.6	229	1 BCLX_CHICK	Q07816 gallus galli
5	428.5	42.5	233	1 BCLX_PIG	O77737 sus scrofa
6	425.5	42.2	233	1 BCLX_MOUSE	Q64373 mus musculus
7	425.5	42.2	233	1 BCLX_RAT	P53563 rattus norv
8	424.5	42.1	233	1 BCLX_HUMAN	Q07817 homo sapien
9	420.5	41.7	233	1 BCL2_CHICK	Q00709 gallus galli
10	412.5	40.9	229	1 BCL2_BOVIN	O02718 bos taurus
11	410	40.6	236	1 BCL2_RAT	P49950 rattus norv
12	409	40.5	236	1 BCL2_MOUSE	P10417 mus musculus
13	408.5	40.5	239	1 BCL2_HUMAN	P10415 homo sapien
14	399	39.5	236	1 BCL2_CRILO	Q93918 cricetus
15	366	36.3	204	1 AR11_XENLA	Q91828 xenopus lae
16	175.5	17.4	208	1 BAK_MOUSE	O08734 mus musculus
17	174	17.2	211	1 BAK_HUMAN	Q16611 homo sapien
18	169	16.7	211	1 BAK2_HUMAN	Q13014 homo sapien
19	156.5	15.5	192	1 BAXA_MOUSE	Q07813 mus musculus
20	155.5	15.4	192	1 BAXA_RAT	Q63690 rattus norv
21	154	15.3	192	1 BAXA_HUMAN	Q07812 homo sapien
22	154	15.3	280	1 CED9_CAEEL	P41958 caenorhabdi
23	148	14.7	192	1 BAXA_BOVIN	O02703 bos taurus
24	147.5	14.6	218	1 BAXB_HUMAN	Q07814 homo sapien
25	144	14.3	177	1 NR13_COTJA	Q90343 coturnix cc
26	140.5	13.9	271	1 CED9_CAEBR	P41957 caenorhabdi
27	138.5	13.7	143	1 BAXD_HUMAN	P55269 homo sapien
28	119	11.8	175	1 BFL1_HUMAN	Q16548 homo sapien
29	116	11.5	350	1 MCL1_HUMAN	Q07820 homo sapien
30	115	11.4	194	1 BCLB_HUMAN	Q9hd36 homo sapien
31	105	10.4	172	1 BFL1_MOUSE	Q07440 mus musculus
32	99.5	9.9	179	1 EAR_ASFV2	Q07819 african swi
33	98.5	9.8	179	1 EAR_ASFB7	P42485 african swi

RESULT 1  
BCLW\_MOUSE  
ID BCLW\_MOUSE STANDARD; PRT; 193 AA.  
AC P70345;  
DI 01-NOV-1997 (Rel. 35, Created)  
DI 01-NOV-1997 (Rel. 35, Last sequence update)  
DI 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-W (BCL2-like 2 protein).  
GN BCL2L2 OR BCLW.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358615; PubMed=8761287;  
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,  
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.;  
RT "Bcl-w, a novel member of the bcl-2 family, promotes cell survival.";  
RL Oncogene 13:665-675(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/10J;  
RX MEDLINE=98160183; PubMed=9500547;  
RA Ross A.J., Waymire K.G., Moss J.E., Parlow A.F., Skinner M.K.,  
RA Russell L.D., Macgregor G.R.;  
RT "Testicular degeneration in Bclw-deficient mice.";  
RL Nat. Genet. 18:251-256(1998).  
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
AND SALIVARY GLAND.  
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
FUNCTION.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
-----  
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-----  
EMBL; U59746; AAB09056.1; -.  
EMBL; AF030769; AAB86430.1; -.  
HSSP; Q07817; IMAZ.  
MGD; MG1:108052; Bcl2l2.  
InterPro; IPR000712; Bcl2\_BH.  
InterPro; IPR003093; Bcl2\_BH4.  
InterPro; IPR002475; BCL2\_family.  
Pfam; PFC0452; Bcl-2; 1.

ALIGNMENTS

34	98.5	3.8	179	1	EAR_ASFE4	Q07818 african swi
35	87.5	8.7	660	1	SQHC_BRAJA	P54924 bradyrhizob
36	86.5	8.6	3433	1	POLG_KUNJM	P14335 k genome po
37	86	8.5	275	1	DAPB_AGR75	Q8uiv8 agrobacteri
38	84.5	8.4	358	1	GLNA_LACSA	P23712 iactuca sat
39	83.5	8.3	872	1	SYA_STRPN	Q97g48 streptococc
40	82.5	8.2	3430	1	POLG_WNV	P06935 w genome po
41	81.5	8.1	887	1	A4_DROME	P14599 drosophila
42	80.5	8.0	236	1	YJ94_ARCFU	Q28285 archaeoglob
43	79	7.8	396	1	PORA_PYRFU	Q51804 pyrococcus
44	79	7.8	454	1	YB48_MYCTU	O06548 mycobacteri
45	79	7.8	454	1	YJ45_MYCTU	P95269 mycobacteri

DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS00063; BH4\_2; 1.  
KW Apoptosis.  
FT DOMAIN 9 29 BH4.  
FT DOMAIN 85 104 BH1.  
FT DOMAIN 136 151 BH2.  
SQ SEQUENCE 193 AA; 20790 MW; 36CA185F5945DFB4 CRC64;  
  
Query Match 99.7%; Score 1006; DB 1; Length 193;  
Best Local Similarity 99.5%; Pred. No. 4.2e-83;  
Matches 192; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MATPASTPDTRALVADFVGRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
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Db 1 MATPASTPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 61 FSDLAALHVTPTGSAQORFTQVSDDELFOGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
|||  
Db 61 FSDLAALHVTPTGSAQORFTQVSDDELFOGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
  
QY 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
|||  
Db 121 QVQDMWVAYLETRLDWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGAVAL 180  
  
QY 181 GALVTVGAFASK 193  
|||  
Db 181 GALVTVGAFASK 193  
  
RESULT 2  
BCLW HUMAN STANDARD; PRT; 193 AA.  
ID BCLW HUMAN  
AC Q92843;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Apoptosis regulator Bcl-w (BCL2-like 2 protein).  
GN BCL2L2 OR BC1W OR KIAA0271.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]\_  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96358615; PubMed=8761287;  
RA Gibson L., Holmgreen S.P., Huang D.C., Bernard O., Copeland N.G.,  
RA Jenkins N.A., Sutherland G.R., Baker E., Adams J.M., Cory S.,  
RT "bcl-w, a novel member of the bcl-2 family, promotes cell survival."  
RL Oncogene 13:665-675(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97191544; PubMed=9039502;  
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,  
RA Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
RT "Prediction of the coding sequences of unidentified human genes. VI.  
RT The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by  
RT analysis of cDNA clones from cell line KG-1 and brain."  
RL DNA Res. 3:321-329(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Stapleton M., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska J., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
CC -!- FUNCTION: PROMOTES CELL SURVIVAL.  
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ALMOST ALL MYELOID CELL LINES AND  
CC IN A WIDE RANGE OF TISSUES, WITH HIGHEST LEVELS IN BRAIN, COLON,  
CC AND SALIVARY GLAND.  
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
CC FUNCTION.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC -----  
DR EMBL; U59747; AAB09055.1; -.  
DR EMBL; D87461; BAA19666.1; -.  
DR EMBL; BC021198; AAH21198.1; -.  
DR HSSP; Q07817; 1MAZ.  
DR MIM; 601931; -.  
DR GO; GO:0038189; F:apoptosis inhibitor activity; TAS.  
DR GO; GO:0036916; P:anti-apoptosis; TAS.  
DR GO; GO:0007283; P:spermatogenesis; TAS.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS00063; BH4\_2; 1.  
KW Apoptosis.  
FT DOMAIN 9 29 BH4.  
FT DOMAIN 85 104 BH1.  
FT DOMAIN 136 151 BH2.  
SQ SEQUENCE 193 AA; 20774 MW; 3792243A50281761 CRC64;  
  
Query Match 98.8%; Score 997; DB 1; Length 193;  
Best Local Similarity 98.4%; Pred. No. 2.7e-82;  
Matches 190; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
  
QY 1 MATPASTPDTRALVADFVGRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
|||  
Db 1 MATPASAPDTRALVADFVGKLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEFETRFRRT 60  
  
QY 61 FSDLAALHVTPTGSAQORFTQVSDDELFOGPNWGRLVAFVFGAALCAESVNKEMEPLVG 120  
|||

Db 61 FSDLAAQLHVTGPSAQORFTQVSDSELFQGGPNWGRJLVAFFVFGAALCAESVKNKEMEPLVG 120  
QY 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGVAL 180  
Db 121 QVQDMWVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGVAL 180  
QY 181 GALVTVGGAFFASK 193  
Db 181 GALVTVGGAFFASK 193

RESULT 3  
ARI\_XENLA  
ID ARI\_XENLA STANDARD; PRT; 228 AA.  
AC Q91827;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator R1 (XR1) (Fragment).  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM: N.A.  
RC TISSUE=Head;  
RX MEDLINE=95331613; PubMed=7607538;  
RA Cruz-Reyes J., Tata J.R.;  
RT "Cloning, characterization and expression of two Xenopus bcl-2-like  
cell-survival genes."  
RL Gene 158:171-179(1995).  
CC -!- FUNCTION: COULD BE THE HOMOLOG OF MAMMALIAN BCL-W.  
CC -!- SUBCELLULAR LOCATION: Membrane-bound (Potential).  
CC -!- DEVELOPMENTAL STAGE: DEVELOPMENTAL REGULATION ONLY OCCURS IN THE  
CC BRAIN OF MID-METAMORPHOSIC TO POST-METAMORPHOSIC TADPOLES AND  
CC ADULTS, WHERE AN INCREASE OF SEVERAL FOLD HAS BEEN OBSERVED.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC -----  
DR EMBL; X82462; CAA57845.1; -  
DR HSP; Q07817; 1MAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
KW Apoptosis; Transmembrane.  
FT NON\_TER 1  
FT DOMAIN 120 139 BH1.  
FT DOMAIN 171 186 BH2.  
FT TRANSMEM 207 227 POTENTIAL.  
SQ SEQUENCE 228 AA; 25068 MW; C499D449A585F8A9 CRC64;

Query Match 64.2%; Score 647.5; DB 1; Length 228;  
Best Local Similarity 57.9%; Pred. No. 5.1e-51;  
Matches 125; Conservative 21; Mismatches 35; Indels 3; Gaps 1;  
QY 10 TRALVDFVGYRLRQKGYVCGAGPGEGPAADPLHQAMRAAGDEPETFRRTFSDLAAQLH 69

Db 48 SRALVEDLVRYKLCQSRSLV---PEPSGAASCALHSAMRAAGDEFERFRQAFSEISTQIH 104  
QY 70 VTPGSAQORFTQVSDSELFQGGPNWGRJLVAFFVFGAALCAESVKNKEMEPLVGQVQDMWVAY 129  
Db 105 VTPGTAYARFAEVAGSLFQGGVNWGRIVAFFVFGAALCAESVKNKEMSPLLPRIQDMWVTY 164  
QY 130 LETRLADWIHSSGGWAEFTALYGDGALEEARLRREGNWSVRTVLTGVALGALVTVGAF 189  
Db 165 LETNLRDWIQSNGGNGFLTYGDGAIEEARRQREGNWSLKTVLTGVALGALMTVGAL 224  
QY 190 FASK 193  
Db 225 FASK 228  
RESULT 4  
BCLX\_CHICK  
ID BCLX\_CHICK STANDARD; PRT; 229 AA.  
AC Q07816; Q98908;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).  
GN BCL2L1 OR BCLX OR BCL-X.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM SHORT).  
RX MEDLINE=93364977; PubMed=8358789;  
RA Boise L.H., Gonzalez-Garcia M., Postema C.E., Ding L., Lindsten T.,  
RA Turka L.A., Mao X., Nunez G., Thompson C.B.;  
RA "bcl-x, a bcl-2-related gene that functions as a dominant regulator  
of apoptotic cell death."  
RL Cell 74:597-608(1993).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM LONG).  
RC STRAIN=Hubbard White Mountain; TISSUE=Testis;  
RX MEDLINE=97264485; PubMed=9110311;  
RA Vilagrasa X., Mezquita C., Mezquita J.;  
RT "Differential expression of bcl-2 and bcl-x during chicken  
spermatogenesis."  
RL Mol. Reprod. Dev. 47:26-29(1997).  
CC -!- FUNCTION: DOMINANT REGULATOR OF APOPTOTIC CELL DEATH. THE LONG  
CC FORM DISPLAYS CELL DEATH REPRESSOR ACTIVITY, WHEREAS THE SHORT  
CC ISOFORM PROMOTES APOPTOSIS (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANES AND PERINUCLEAR  
CC ENVELOPE (BY SIMILARITY).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=Q07816-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=Q07816-2; Sequence=VSP\_000514;  
CC -!- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ORGANS WITH LYMPHOID  
CC DEVELOPMENT.  
CC -!- DOMAIN: BH4 DOMAIN SEEMS TO BE INVOLVED IN THE ANTI-APOPTOTIC  
CC FUNCTION. INTACT BH1 AND BH2 DOMAINS ARE REQUIRED FOR ANTI-  
CC APOPTOTIC ACTIVITY (BY SIMILARITY).  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC -----  
DR EMBL; Z23110; CAA08657.1; -.  
DR EMBL; U26645; AABC7677.1; -.  
DR PIR; A47537; A47537.  
DR HSSP; P53563; 1AF3.  
DR InterPro; IPR000712; Bcl2 BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1\_1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS01260; BH4\_2; 1.  
DR PROSITE; PS00063; BH4\_2; 1.  
KW Apoptosis; Transmembrane; Alternative splicing.  
FT DOMAIN 4 24 BH4.  
FT DOMAIN 82 96 BH3.  
FT DOMAIN 125 144 BH1.  
FT DOMAIN 176 191 BH2.  
FT TRANSMEM 206 223  
FT VARSPIC 185 229 POTENTIAL.  
FT ERFVDLYGNNAALRLKQGETFNKWLITGATVAGVLLGLSL  
FT LSRK -> VRTALP (in isoform Short).  
FT /FTId=VSP\_000514.  
FT SEQUENCE 229 AA; 25733 MW; A97D3A4D04C0E9DA CRC64;  
QY Query Match 42.6%; Score 429.5; DB 1; Length 229;  
Best Local Similarity 41.2%; Pred. No. 2e-31;  
Matches 94; Conservative 23; Mismatches 62; Indels 49; Gaps 4;  
D5 11 RALVADFVGYRLRQKY-----VCGAGPGEGP----- 37  
D5 6 RELVIDFVSXKLSQRGHCWSELEEBDENRTDTAAEAEMDSVLNCSFSPHPPAGHVVGAT 65  
QY 38 -----AADPLHQAMRAAGDEFETPRRTFSCLAAQLHVTGSAQQRFTQVSDE 95  
D5 66 VHRSSLEVEHIVRASDVQRALRDAGDEFELRYRRAFSDLTSQLH:TPGTAYQSFEQVYNE 125  
QY 86 LFQGGPNWGRVAVFFVFGAALCAESVKNKEMPLVGQVQDMVAVYETRLADWIHSSGGWA 145  
D5 126 LFHDGVNWGRVAVFFSFGGALCVESVKEMRVLVGRIVSWMTTITDHLDPWIQENGWE 185  
QY 146 EFTALYGDGALEEARLRREGNWASVRTVLTGAVALGALVTVGAFASK 193  
D5 186 RFVDLYGNNA---AAELRKQGETFNKWLITGATVAGVLL-LGSLLSRK 229  
RESULT 5  
BCLX\_PIG STANDARD; PRT; 233 AA.  
AC O77737;  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-JUL-1999 (Rel. 38, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Apoptosis regulator Bcl-X (BCL2-like 1 protein).  
GN BCL2L1 OR BCL2L OR BCLX.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99171363; PubMed=10072723;  
RA Bartling B., Hoffmann J., Holtz J., Schulz R., Heusch G., Darmer D.;  
RT "Quantification of cardioprotective gene expression in porcine  
RT short-term hibernating myocardium.";

RL U. Mol. Cell. Cardiol. 31:147-158(1999).  
CC -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-  
CC apoptotic activity is inhibited by association with SIVA isoform  
CC 1. Inhibits activation of caspases (By similarity). Appears to  
CC regulate cell death by blocking the voltage-dependent anion  
CC channel (VDAC) by binding to it and preventing the release of the  
CC caspase activator, cytochrome c, from the mitochondrial membrane.  
CC -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By  
CC similarity). Heterodimerization with BAX does not seem to be  
CC required for anti-apoptotic activity (By similarity). Isoform Bcl-  
CC x(L) binds to Siva isoform 1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear  
CC envelope (By similarity).  
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.  
CC The BH1 and BH2 domains are required for both heterodimerization  
CC with other Bcl2 family members and for repression of cell death.  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis (By  
CC similarity). The cleaved protein, lacking the BH4 domain, has pro-  
CC apoptotic activity (By similarity).  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).  
CC -----  
CC EMBL; AJ001203; CAA04597.1; -.  
DR HSSP; Q07817; 1MAZ.  
DR InterPro; IPR000712; Bcl2 BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1\_1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS00063; BH4\_2; 1.  
KW Apoptosis; Mitochondrion; Transmembrane.  
FT DOMAIN 4 24 BH4.  
FT DOMAIN 86 100 BH3.  
FT DOMAIN 129 148 BH1.  
FT DOMAIN 180 195 BH2.  
FT TRANSMEM 210 226 POTENTIAL.  
SQ SEQUENCE 233 AA; 26061 MW; 18BF6FA041912B2 CRC64;  
Query Match 42.5%; Score 428.5; DB 1; Length 233;  
Best Local Similarity 41.3%; Pred. No. 2.5e-31;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;  
QY 11 RALVADFVGYRLRQKY-----V 28  
D5 6 RELJVDFLSYKLSQKYSWSQFTDVEENRTEAPEGTESEAEPTSPAINGNPSWHLADSPAV 65  
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETPRRTFSCLAAQLHVTGSAQQRFT 80  
D5 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124  
QY 81 QVSDELFQGGPNWGRVAVFFVFGAALCAESVKNKEMPLVGQVQDMVAVYETRLADWIHS 140  
D5 125 QVLNELFRDGVNWGRVAVFFSFGGALCVESVDKEMQVLVSRIATWMATYLNHLEPWIQE 184

```
QY      141 SGGWAEFTALYGDGALEEARRLRE--GNWASVRTVLTGAVALGAL 183
      :||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Db      185 NGGWDTFVELYGNNAASERKQGERFNRFLTGMTLAGVVLGSL 229

RESULT 6
BCLX_MOUSE
ID      BCLX_MOUSE      STANDARD;      PRT;      233 AA.
AC      Q64373; Q60657; Q60658; Q61338;
DT      01-NOV-1997 (Rel. 35, Created)
DI      01-NOV-1997 (Rel. 35, Last sequence update)
DI      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Apoptosis regulator Bcl-x (BCL2-like 1 protein).
GN      BCL2L1 OR BCL2L OR BCLX.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=2A4B;
RA      Kamesaki H., Michaud G.Y., Takatsu K., Okuma M.;
RL      Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=95331139; PubMed=7607090;
RA      Gonzalez-Garcia M., Perez-Ballester R., Ding L., Duan L., Boise L.H.,
RA      Thompson C.B., Nunez G.;
RT      "bcl-XL is the major bcl-x mRNA form expressed during murine
RT      development and its product localizes to mitochondria.";
RL      Development 120:3033-3042(1994).
RN      [3]
RP      SEQUENCE FROM N.A. (ISOFORMS X(L); X(S) AND X(Delta-TM)).
RC      TISSUE=Pre-B cell;
RX      MEDLINE=95052604; PubMed=7963517;
RA      Fang W., Rivard J.J., Mueller D.L., Behrens T.W.;
RT      "Cloning and molecular characterization of mouse bcl-x in B and T
RT      lymphocytes.";
RL      J. Immunol. 153:4388-4398(1994).
RN      [4]
RP      SEQUENCE FROM N.A. (ISOFORM X(BETA)).
RC      STRAIN=C57BL/6 X CBA; TISSUE=Thymus;
RX      MEDLINE=98051053; PubMed=9390687;
RA      Yang X.-F., Weber G.F., Cantor H.;
RT      "A novel Bcl-x isoform connected to the T cell receptor regulates
RT      apoptosis in T cells.";
RL      Immunity 7:629-639(1997).
RN      [5]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=97289584; PubMed=9144489;
RA      Grilhot D.A., Gonzalez-Garcia M., Ekhterae D., Duan L., Inohara N.,
RA      Ohta S., Seldin M.F., Nunez G.;
RT      "Genomic organization, promoter region analysis, and chromosome
RT      localization of the mouse bcl-x gene.";
RL      J. Immunol. 158:4750-4757(1997).
RN      [-]
CC      FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-
CC      apoptotic activity is inhibited by association with SIVA isoform
CC      1. Inhibits activation of caspases (By similarity). Appears to
CC      regulate cell death by blocking the voltage-dependent anion
CC      channel (VDAC) by binding to it and preventing the release of the
CC      caspase activator, cytochrome c, from the mitochondrial membrane.
CC      The Bcl-x(S) isoform promotes apoptosis.
CC      [-] SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC      similarity). Heterodimerization with BAX does not seem to be
CC      required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC      x(L) binds to Siva isoform 1 (By similarity).
CC      [-] SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC      envelope for Bcl-x(L). Cytoplasmic for Bcl-x(delta-TM).
CC      [-] ALTERNATIVE PRODUCTS:
CC      Event=Alternative splicing; Named isoforms=4;
CC      Name=BCX-X(L);
```

```
CC      IsoId=Q64373-1; Sequence=Displayed;
CC      Name=BCL-X(S);
CC      IsoId=Q64373-2; Sequence=VSP_000517;
CC      Name=BCL-X(beta);
CC      IsoId=Q64373-3; Sequence=VSP_000518;
CC      Name=BCL-X(delta-TM);
CC      IsoId=Q64373-4; Sequence=VSP_000519;
CC      [-] TISSUE SPECIFICITY: Widely expressed, with highest levels in the
CC      brain, thymus, bone marrow, and kidney. Bcl-x(L) and Bcl-x(delta-
CC      TM) expression is enhanced in B and T lymphocytes that have been
CC      activated.
CC      [-] DEVELOPMENTAL STAGE: Bcl-x(beta) is expressed in both embryonal
CC      and postnatal tissues, whereas Bcl-x(L) is predominantly found in
CC      postnatal tissues.
CC      [-] DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC      The BH1 and BH2 domains are required for both heterodimerization
CC      with other Bcl2 family members and for repression of cell death.
CC      [-] PTM: Proteolytically cleaved by caspases during apoptosis (By
CC      similarity). The cleaved protein, lacking the BH4 domain, has pro-
CC      apoptotic activity (By similarity).
CC      [-] SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      [-] SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC      [-] SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC      [-] SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC      [-] SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X83574; CAA58557.1; -
DR      EMBL; L35049; AAA51039.1; -
DR      EMBL; J35048; AAA51040.1; -
DR      EMBL; U10102; AAA82174.1; -
DR      EMBL; U10101; AAA82173.1; -
DR      EMBL; U10100; AAA82172.1; -
DR      EMBL; U51279; AAC53460.1; -
DR      EMBL; U78031; AAB96881.1; -
DR      EMBL; U78030; AAB96881.1; JOINED.
DR      PIR; I49055; I49055.
DR      PIR; I49056; I49056.
DR      PIR; I49057; I49057.
DR      HSSP; P53563; IAF3.
DR      MGD; MGI:88139; Bcl2l.
DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; BCL2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.
DR      SMART; SM00265; BH4; 1.
DR      TIGRFAMs; TIGR00865; bcl-2; 1.
DR      PROSITE; PS50062; BCL2_FAMILY; 1.
DR      PROSITE; PS01080; BH1; 1.
DR      PROSITE; PS01258; BH2; 1.
DR      PROSITE; PS01259; BH3; 1.
DR      PROSITE; PS01260; BH4_1; 1.
DR      PROSITE; PS0063; BH4_2; 1.
KW      Apoptosis; Mitochondrion; Alternative splicing; Transmembrane.
FT      DOMAIN 4 24 BH4.
FT      DOMAIN 86 100 BH3.
FT      DOMAIN 129 148 BH1.
FT      DOMAIN 180 195 BH2.
FT      TRANSMEM 210 226 POTENTIAL.
FT      VARSPPLIC 126 188 Missing (in isoform BCL-X(S)).
FT      VARSPPLIC 189 233 /FTId=VSP_000517.
FT      DTFVDLYGNNAASERKQGERFNRFLTGMTVAGVVLGSL
FT      FSRK -> VRTTPLVCPPLACVSLCEHP (in isoform
```

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FT      BCL-X(beta)).
FT      /FTid=VSP_000518.
FT      LYGNNAAEFSRKQERFNWFLTGMTVAGVWLLGSLFSRK
FT      -> GHDCGWCGSAGLTLQSEVTRH (in isoform
FT      BCL-X(delta-TM)).
FT      /FTid=VSP_000519.
SQ      SEQUENCE 233 AA; 26132 MW; 24D2AC79687E072E CRC64;

Query Match      42.2%; Score 425.5; DB 1; Length 233;
Best Local Similarity 40.9%; Pred. No. 4.6e-31;
Matches 92; Conservative 23; Mismatches 57; Indels 53; Gaps 4;

QY      11  RALVADFVGYRLPQKGY-----V 28
           ||| ||| ||| ||| |||
Db       6  RELVDFLSYKLSCKGYSWQSFSDVEENRTEAPEETEAERETPTSAINGNPSWHJADSPAV 65
           : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      29  CGAGPGEGPAAD-----PLHQAVRAAGDEFETRFRRTESDLAAQLHVTGSAQQQRF 80
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       66  NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124
           : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      81  QVSDELFOGGPNWGRVLVAFVFGAALCAESVNKEMEFLVGQVQDMVYAYLETRLADWIHS 140
           ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       125 QVWNEFLRDGVNWGRIVAFVFGGALCVESVDKEMQVLSVRIASWNAATYLNHLEPWIOE 184
           : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY      141 SGGWAEFTALYGDGALDEEARLRE--GNWASVRTVLTGAVALGAL 183
           : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db       185 NGGWDTFVDLYGNNAAEFSRKQERFNWFLTGMTVAGVWLLGSL 229
           : ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 7
BCLX_RAT      STANDARD; PRT; 233 AA.
ID            P70614; Q62678; Q62836; Q64087; Q64128;
AC            P53563; P70613; P70614; Q62678; Q64087; Q64128;
DT            01-OCT-1996 (Rel. 34, Created)
DT            01-NOV-1997 (Rel. 35, Last sequence update)
DT            15-SEP-2003 (Rel. 42, Last annotation update)
DE            Apoptosis regulator Bcl-X (BCL2-like 1 protein).
GN            BCL2L1 OR BCL2L OR BCLX.
OS            Rattus norvegicus (Rat).
OC            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX            NCBI_TaxID=10116;
RN            [1]
RP            SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC            TISSUE=Brain;
RA            Michaelidis T.M.;
RL            Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN            [2]
RP            SEQUENCE FROM N.A.
RC            TISSUE=Brain;
RA            Wesselingh S.L., Choi S., Veliuona M., Hardwick C.M.;
RL            Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN            [3]
RP            SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(BETA)).
RC            TISSUE=Thymus;
RX            MEDLINE=96278736; PubMed=8662675;
RA            Shiraiwa N., Inohara N., Okada S., Yuzaki M., Shoji S.-I., Ohta S.;
RT            "An additional form of rat Bcl-x, Bcl-xbeta, generated by an
RT            unspliced RNA, promotes apoptosis in promyeloid cells.";
RJ            J. Biol. Chem. 271:13258-13265(1996).
RN            [4]
RP            SEQUENCE FROM N.A. (ISOFORMS X(L) AND X(S)).
RC            STRAIN=Sprague-Dawley; TISSUE=Ovary;
RX            MEDLINE=95129487; PubMed=7828536;
RA            Tilly J.L., Tilly K.I., Kenton M.L., Johnson A.L.;
RT            "Expression of members of the bcl-2 gene family in the immature rat
RT            ovary: equine chorionic gonadotropin-mediated inhibition of granulosa
RT            cell apoptosis is associated with decreased bax and constitutive
RT            bcl-2 and bcl-xl-long messenger ribonucleic acid levels.";
RL            Endocrinology 136:232-241(1995).
RN            [5]
RP            X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX            MEDLINE=98010630; PubMed=9346936;
```

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RA      Aritomi M., Kunishima N., Inohara N., Ishibashi Y., Ohta S.,
RA      Morikawa K.;
RT      "Crystal structure of rat Bcl-xL. Implications for the function of
RT      the Bcl-2 protein family.";
RL      J. Biol. Chem. 272:27886-27892(1997).
CC      -!- FUNCTION: Potent inhibitor of cell death. Isoform Bcl-x(L) anti-
CC      apoptotic activity is inhibited by association with SIVA isoform
CC      i. Inhibits activation of caspases (By similarity). Appears to
CC      regulate cell death by blocking the voltage-dependent anion
CC      channel (VDAC) by binding to it and preventing the release of the
CC      caspase activator, cytochrome c, from the mitochondrial membrane.
CC      The Bcl-x(S) and Bcl-x(beta) isoforms promote apoptosis.
CC      -!- SUBUNIT: Bcl-x(L) forms heterodimers with BAX, BAK and Bcl-2 (By
CC      similarity). Heterodimerization with BAX does not seem to be
CC      required for anti-apoptotic activity (By similarity). Isoform Bcl-
CC      x(L) binds to Siva isoform 1 (By similarity).
CC      -!- SUBCELLULAR LOCATION: Mitochondrial membranes and perinuclear
CC      envelope (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC      Name=Alternative splicing; Named isoforms=3;
CC      Name=Bcl-X(L);
CC      IsoId=P53563-1; Sequence=Displayed;
CC      Name=Bcl-X(S);
CC      IsoId=P53563-2; Sequence=VSP_000520;
CC      Name=Bcl-X(beta);
CC      IsoId=P53563-3; Sequence=VSP_000521;
CC      -!- TISSUE SPECIFICITY: Expressed in most tissues. Bcl-x(beta) is
CC      specifically expressed in cerebellum, heart, and thymus. In the
CC      ovary, the predominant form is Bcl-x(L), with a small but
CC      detectable level of Bcl-x(S).
CC      -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity.
CC      The BH1 and BH2 domains are required for both heterodimerization
CC      with other Bcl2 family members and for repression of cell death.
CC      -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC      cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC      activity (By similarity).
CC      -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC      -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC      -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC      -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
CC      -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC      -----
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CC      -----
DR      EMBL; X82537; CAA57886.1; -
DR      EMBL; X82537; CAA57887.1; -
DR      EMBL; U10579; AAA19257.1; -
DR      EMBL; U72350; AAB17353.1; -
DR      EMBL; U72349; AAB17352.1; -
DR      EMBL; U34963; AAA77686.1; -
DR      EMBL; S76513; AAC60701.1; ALT_INIT.
DR      EMBL; S78284; AAC60702.1; -
DR      PIR; I67431; I67431.
DR      PIR; S51761; S51761.
DR      PDB; 1AF3; 07-JUL-97.
DR      InterPro; IPR000712; Bcl2_BH.
DR      InterPro; IPR003093; Bcl2_BH4.
DR      InterPro; IPR002475; BCL2_family.
DR      InterPro; IPR004725; Bcl2_reg.
DR      Pfam; PF00452; Bcl-2; 1.
DR      Pfam; PF02180; BH4; 1.
DR      SMART; SM00337; BCL; 1.
DR      SMART; SM00265; BH4; 1.
DR      TIGRFAMs; TIGR00865; bcl-2; 1.
DR      PROSITE; PS50062; BCL2_FAMILY; 1.
DR      PROSITE; PS01080; BH1; 1.
DR      PROSITE; PS01258; BH2; 1.
```













CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC Dephosphorylated by protein phosphatase 2A (PP2A) (By similarity).  
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol  
CC promoting further caspase activity (By similarity).  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC -----  
CC EMBL; L14680; AAA53662.1; -  
CC EMBL; U34964; AAA77687.1; -  
CC EMBL; S74122; -; NOT\_ANNOTATED\_CDS.  
CC PIR; I53744; I53744.  
CC PIR; I67432; I67432.  
CC HSSP; Q07817; IMAZ.  
CC InterPro; IPR000712; Bcl2 BH.  
CC InterPro; IPR003093; Bcl2\_BH4.  
CC InterPro; IPR02475; BCL2 family.  
CC InterPro; IPR004725; Bcl2\_reg.  
CC Pfam; PF00452; Bcl-2; 1.  
CC Pfam; PF02180; BH4; 1.  
CC SMART; SM00337; BCL; 1.  
CC SMART; SM00265; BH4; 1.  
CC TIGRFAMs; TIGR00865; bcl-2; 1.  
CC PROSITE; PS00662; BCL2\_FAMILY; 1.  
CC PROSITE; PS01080; BH1; 1.  
CC PROSITE; PS01258; BH2; 1.  
CC PROSITE; PS01259; BH3; 1.  
CC PROSITE; PS01260; BH4\_1; 1.  
CC PROSITE; PS00663; BH4\_2; 1.  
KW Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.  
FT DOMAIN 10 30 BH4.  
FT DOMAIN 90 104 BH3.  
FT DOMAIN 133 152 BH1.  
FT DOMAIN 184 199 BH2.  
FT TRANSMEM 209 230 POTENTIAL.  
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).  
FT CONFLICT 42 42 A -> R (IN REF. 2).  
FT CONFLICT 157 157 E -> G (IN REF. 1).  
FT CONFLICT 164 164 S -> Y (IN REF. 2).  
FT CONFLICT 212 212 L -> Q (IN REF. 2).  
SQ SEQUENCE 236 AA; 26622 MW; E7688CB9071A872A CRC64;  
  
Query Match 40.6%; Score 410; DB 1; Length 236;  
Best Local Similarity 35.8%; Pred. No. 1.le-29;  
Matches 83; Conservative 35; Mismatches 62; Indels 52; Gaps 3;  
  
Qy 9 DTRALVADFVGYRLRQKY----- 27  
Db 10 DNRIVMKYIHYKLSQGVYWDGTGDEDSAPLRAAFTPGIFSPQESNRTPAVHRDTAART 69  
Qy 28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETFRRTFSDLAAQLHVTGSAQQRFTQ 81  
Db 70 SPRLPLVANAGPALSPVPVHILTLRRAGDDESRVYRDDFAEXSSQLHLTPFTARGFAT 129  
Qy 82 VSDELFGQGNWGRVLVAFFVFGAALCAESVNKEMEPVLGVQVQDMVAYLETRLADWHS 141  
Db 130 VVEELFRDGVNWGRIVAFFEFGVMCVESVNREMSPLVDNIALWMTEYLNPRHLHTWQDN 169

Qy 142 GGWAFTALYGDGGALEBARRLRGNWASVRTLTGAVLGTGVAFFASK 193  
Db 190 GGWDAFVELYG-----PSMRPLDFSWLSKTLTSLAL-VGACITLGAYLGHK 236  
  
RESULT 12  
BCL2\_MOUSE  
ID BCL2\_MOUSE STANDARD; PRT; 236 AA.  
AC P10417; P10418;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2 OR BCL-2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RC STRAIN=BALB/c; TISSUE=Liver;  
RX MEDLINE=87187643; PubMed=3032455;  
RA Negrini M., Silini E., Kozak C., Tsujimoto Y., Croce C.M.;  
RI "Molecular analysis of mbcl-2: structure and expression of the murine  
RI gene homologous to the human gene involved in follicular lymphoma."  
RI Cell 49:455-463(1987).  
RN [2]  
RP REVISIONS TO 221-222.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
RI "Isolation and characterization of the chicken bcl-2 gene: expression  
RI in a variety of tissues including lymphoid and neuronal organs in  
RI adult and embryo."  
RI Nucleic Acids Res. 20:4187-4192(1992).  
RN [3]  
RP PHOSPHORYLATION BY PKC, AND MUTAGENESIS OF SERINE RESIDUES.  
RX MEDLINE=97277291; PubMed=9115213;  
RA Ito T., Deng X., Carr B., Mumby M., May W.S. Jr.;  
RI "Bcl-2 phosphorylation required for anti-apoptosis function."  
RI J. Biol. Chem. 272:11671-11673(1997).  
RN [4]  
RP DEPHOSPHORYLATION BY PP2A.  
RX MEDLINE=99069407; PubMed=9852076;  
RA Deng X., Ito T., Carr B., Mumby M., May W.S. Jr.;  
RI "Reversible phosphorylation of Bcl2 following interleukin 3 or  
RI bryostatine 1 is mediated by direct interaction with protein  
RI phosphatase 2A\*."  
RI J. Biol. Chem. 273:34157-34163(1998).  
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems  
CC including factor-dependent lymphohematopoietic and neural cells.  
CC Regulates cell death by controlling the mitochondrial membrane  
CC permeability. Appears to function in a feedback loop system with  
CC caspases. Inhibits caspase activity either by preventing the  
CC release of cytochrome c from the mitochondria and/or by binding to  
CC the apoptosis-activating factor (APAF-1).  
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and  
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2  
CC domains, and is necessary for anti-apoptotic activity (By  
CC similarity). Also interacts with APAF-1 and RAF-1.  
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular  
CC membrane of the nuclear envelope and the endoplasmic reticulum.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Alpha;  
CC IsoId=P10417-1; Sequence=Displayed;  
CC Name=Beta;  
CC IsoId=P10417-2; Sequence=VSP\_000513;  
CC -!- TISSUE SPECIFICITY: Expressed in a variety of tissues.  
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and  
CC for interaction with RAF-1.  
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2  
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation  
CC on Ser-70 by PKC is required for the anti-apoptosis activity and



CC occurs during the G2/M phase of the cell cycle. In the absence of  
CC growth factors, Bcl2 appears to be phosphorylated by other protein  
CC kinases such as ERKs and stress-activated kinases.  
CC Dephosphorylated by protein phosphatase 2A (PP2A).  
CC -!- PTX: Proteolytically cleaved by caspases during apoptosis. The  
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic  
CC activity, causes the release of cytochrome c into the cytosol  
CC promoting further caspase activity.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.  
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.  
CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; L31532; AAA37282.1; ..  
DR EMBL; M16506; AAA37282.1; JOINED.  
DR EMBL; M16506; AAA37281.1; ..  
DR PIR; B25960; TVMSB1.  
DR HSSP; Q07817; 1MAZ.  
DR MGD; MGI:88138; Bcl2.  
DR GO; GO:0008189; F:apoptosis inhibitor activity; IDA.  
DR GO; GO:0005515; F:protein binding activity; IPI.  
DR GO; GO:0006915; P:apoptosis; IDA.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2 family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS50062; BCL2 FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
KW Apoptosis; Alternative splicing; Transmembrane; Mitochondrion;  
KW Phosphorylation.  
FT DOMAIN 10 30 BH4.  
FT DOMAIN 90 104 BH3.  
FT DOMAIN 133 152 BH1.  
FT DOMAIN 184 199 BH2.  
FT TRANSMEM 209 230 POTENTIAL.  
FT SITE 34 35 CLEAVAGE (BY CASPASES) (BY SIMILARITY).  
FT MOD\_RES 70 70 PHOSPHORYLATION (BY PKC).  
FT VARSPIC 193 236 DAFVELYGPSMRPLPDFSLSLTKTLSSALVGACITLGAY-  
FT GHK -> VGACIVE (in isoform Beta).  
FT /FTid=VSP\_000513.  
SQ SEQUENCE 236 AA; 26425 MW; AA85EF65076CB30A CRC64;  
  
Query Match 40.5%; Score 409; DB 1; Length 236;  
Best Local Similarity 37.1%; Pred. No. 1.4e-29;  
Matches 86; Conservative 35; Mismatches 59; Indels 52; Gaps 5;  
  
QY 9 DTRALVADFVGYRLRQKGYVCGAG-----PG----- 34  
Db 10 DNRRIWMKYIHYKLSQRGYEWADAGDADAAPLGAAPTPTGIFSFQPSNDPMAVHREMAART 69  
QY 35 -----EGPAADP-----LHQAMRAAGDEFETFRRTFSDLAQLHVTGPSAQQRETQ 81  
Db 70 SPLRPLVATAGPALSPVPCVHLTLRRAGDDFSRRYRDRFAEMSSQLHLTPFTARGREAT 129  
QY 82 VSDELFGQGNWGRVLAFFVFGAALCAESVKNEMPLVGQVQDMVAYLETRLADWTHSS 141

Db 130 VVEELFRDGVNWGRIVAFPEFGVMCVESVNRMSPLVDNIALWMTEYLNRLHHTWIQDN 189  
QY 142 GCWAEFTALYGDGALEEARLRREGNWASVRTVLTGVALGALVTVGAFPAASK 193  
Db 190 GCWDADFVELYG----PSMRPLDFSLSLTKTLSSAL-VGACITLGAYLGHK 236  
  
RESULT 13  
BCL2\_HUMAN  
ID BCL2\_HUMAN STANDARD; PRT; 239 AA.  
AC P10415; P10416; Q13842; Q16197;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-SEP-2003 (Rel. 42, Last annotation update)  
DE Apoptosis regulator Bcl-2.  
GN BCL2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).  
RX MEDLINE=86259760; PubMed=3523487;  
RA Tsujimoto Y., Croce C.M.;  
RT "Analysis of the structure, transcripts, and protein products of  
RT bcl-2, the gene involved in human follicular lymphoma.";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:5214-5218(1986).  
RN [2]  
RP REVISIONS TO 96; 110 AND 237.  
RX MEDLINE=92375724; PubMed=1508712;  
RA Eguchi Y., Ewert D.L., Tsujimoto Y.;  
RT "Isolation and characterization of the chicken bcl-2 gene: expression  
RT in a variety of tissues including lymphoid and neuronal organs in  
RT adult and embryo.";  
RL Nucleic Acids Res. 20:4187-4192(1992).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=87002488; PubMed=2875799;  
RA Cleary M.L., Smith S.D., Sklar J.;  
RT "Cloning and structural analysis of cDNAs for bcl-2 and a hybrid bcl-  
RT 2/immunoglobulin transcript resulting from the t(14;18)  
RT translocation.";  
RL Cell 47:19-28(1986).  
RN [4]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RX MEDLINE=88196071; PubMed=2834197;  
RA Seto M., Jaeger U., Hockett R.D., Graninger W., Bennett S.,  
RA Goldman P., Korsmeyer S.J.;  
RT "Alternative promoters and exons, somatic mutation and deregulation  
RT of the Bcl-2-Ig fusion gene in lymphoma.";  
RL EMBO J. 7:123-131(1988).  
RN [5]  
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).  
RT ISSUE=Testis;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Heiton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;



```
QY 36 -----GPAADP-----LHQAMRAAGDEFTFRRTFSDLAQLHVTGPSAQQR 78
D 70 SPLQTPAAPGAAGPALSPVPVWHLTLRQAGDDFSRRYRRDFAEMSSQLHLTPFTARGR 129
QY 79 FTQVSDLELFOGPNWGRJLVAFVFGAALCAESVNMKEPVLVGQVQDMVWVAYLETRLADWI 138
D 130 FATVVEELFRDGVNWRIVAFVFGGVMCVESVNREMSPLVDNIALWTEYLNRLHHTWI 189
QY 139 HSSGGWAEFTALYGDGALEEARLRREGNWSVTRVLTGAVALGALVTVGAFFASK 193
D 190 QDNGGWDAFVELYG-----PSMRPLDFFSWLSLTKLLSLAL-VGACITLGGAYLGHK 239

RESULT 14
BCL2_CRILO
ID BCL2_CRILO STANDARD; PRT; 236 AA.
AC Q9JJV8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator Bcl-2.
GN BCL2.
OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Cricetulus.
OX NCBI_TaxID=10030;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Ovary;
RX MEDLINE=20431763; PubMed=10973819;
RA Tomicic M.T., Christmann M., Kaina B.;
RT "Cloning and functional analysis of cDNA encoding the hamster Bcl-2
RL protein."
RL Biochem. Biophys. Res. Commun. 275:899-903(2000).
RN [2]
RP SEQUENCE FROM N.A., AND CLEAVAGE BY CASPASES.
RX MEDLINE=21092839; PubMed=1181062;
RA Tomicic M.T., Kaina B.;
RT "Hamster Bcl-2 protein is cleaved in vitro and in cells by caspase-9
RL and caspase-3."
RL Biochem. Biophys. Res. Commun. 281:404-408(2001).
CC -!- FUNCTION: Suppresses apoptosis in a variety of cell systems
CC including factor-dependent lymphohematopoietic and neural cells.
CC Regulates cell death by controlling the mitochondrial membrane
CC permeability. Appears to function in a feedback loop system with
CC caspases. Inhibits caspase activity either by preventing the
CC release of cytochrome c from the mitochondria and/or by binding to
CC the apoptosis-activating factor (APAF-1) (By similarity).
CC -!- SUBUNIT: Forms homodimers, and heterodimers with BAX, BAD, BAK and
CC Bcl-x(L). Heterodimerization with BAX requires intact BH1 and BH2
CC domains, and is necessary for anti-apoptotic activity (By
CC similarity). Also interacts with APAF-1 and RAF-1 (By similarity).
CC -!- SUBCELLULAR LOCATION: Outer mitochondrial membrane, intracellular
CC membrane of the nuclear envelope and the endoplasmic reticulum.
CC -!- DOMAIN: The BH4 domain is required for anti-apoptotic activity and
CC for interaction with RAF-1 (By similarity).
CC -!- PTM: Phosphorylation/dephosphorylation on Ser-70 regulates Bcl2
CC anti-apoptotic activity. Growth factor-stimulated phosphorylation
CC on Ser-70 by PKC is required for the anti-apoptosis activity and
CC occurs during the G2/M phase of the cell cycle (By similarity). In
CC the absence of growth factors, Bcl2 appears to be phosphorylated
CC by other protein kinases such as ERKs and stress-activated kinases
CC (By similarity). Dephosphorylated by protein phosphatase 2A (PP2A)
CC (By similarity).
CC -!- PTM: Proteolytically cleaved by caspases during apoptosis. The
CC cleaved protein, lacking the BH4 domain, has pro-apoptotic
CC activity, causes the release of cytochrome c into the cytosol
CC promoting further caspase activity.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 1 (BH1) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 2 (BH2) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 3 (BH3) domain.
CC -!- SIMILARITY: Contains 1 Bcl-2 homology 4 (BH4) domain.
```

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CC -!- SIMILARITY: BELONGS TO THE BCL-2 FAMILY.
CC -----
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CC -----
CC EMBL; AJ271720; CAB92245.1; -.
CC PIR; JC7383; JC7383.
CC HSSP; Q07817; IMAZ.
CC InterPro; IPR000712; Bcl2_BH.
CC InterPro; IPR003093; Bcl2_BH4.
CC InterPro; IPR002475; BCL2_family.
CC InterPro; IPR004725; Bcl2_reg.
CC Pfam; PF00452; Bcl-2; 1.
CC Pfam; PF02180; BH4; 1.
CC SMART; SM00337; BCL; 1.
CC SMART; SM00265; BH4; 1.
CC TIGRFAMs; TIGR00865; bcl-2; 1.
CC PROSITE; PS50062; BCL2_FAMILY; 1.
CC PROSITE; PS01080; BH1; 1.
CC PROSITE; PS01258; BH2; 1.
CC PROSITE; PS01259; BH3; 1.
CC PROSITE; PS01260; BH4; 1; 1.
CC PROSITE; PS50063; BH4_2; 1.
CC Apoptosis; Transmembrane; Mitochondrion; Phosphorylation.
CC DOMAIN 10 30 BH4.
CC DOMAIN 90 104 BH3.
CC DOMAIN 133 152 BH1.
CC DOMAIN 184 199 BH2.
CC TRANSMEM 209 230 POTENTIAL.
CC SITE 64 65 CLEAVAGE (BY CASPASE-3 AND CASPASE-9).
CC MOD_RES 70 70 PHOSPHORYLATION (BY PKC) (BY SIMILARITY).
CC SEQUENCE 236 AA; 26491 MW; BECADFIEF337228 CRC64;

Query Match 39.5%; Score 399; DB 1; Length 236;
Best Local Similarity 34.9%; Pred. No. 1.le-28;
Matches 81; Conservative 35; Mismatches 64; Indels 52; Gaps 3;

QY 9 DTRALVADFVGYRLRQKGY----- 27
D 10 DNREIVMKYIHYKLSQRGYEWDVGDVDAELGAAPTGFISFQPSNPPTPAVHRDMAART 69
QY 28 -----VCGAGPGEGPAADPLHQAMRAAGDEFETRFRRTFSDLAQLHVTGPSAQQRFTQ 81
D 70 SPLRPVATVTGPTLSPVPPVWHLTLRAGDDFSRRYRRDFAEMSSQLHLTPFTARGRFAT 129
QY 82 VSDELFGGPNWGRJLVAFVFGAALCAESVNMKEPVLVGQVQDMVWVAYLETRLADWIHSS 141
D 130 VVEELFRDGVNWRIVAFVFGGVMCVESVNREMSPLVDNIALWTEYLNRLHHTWIQDN 189
QY 142 GGWAEFTALYGDGALEEARLRREGNWSVTRVLTGAVALGALVTVGAFFASK 193
D 190 GGWDAFVELYG-----PSVRPLDFFSWLSLTKLLSLAL-VGACITLGTLYLGHK 236

RESULT 15
ARI--XENLA
ID ARI--XENLA STANDARD; PRT; 204 AA.
AC Q91828;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apoptosis regulator R11 (XR11).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
```

	Query Match	36.3%;	Score 366;	DB 1;	Length 204;
	Best Local Similarity	41.5%;	Pred. No. 8.5e-26;		
	Matches	81;	Conservative	25;	Mismatches 63; Indels 26; Gaps 4;
QY	10	TRALVADFVGRLRQKGYVC-----GAGGEGGPAAJPLHQAMR	47		
		:    :  :	:	:	:
Db	5	SRDLEKFVSCKLSQ-NEACKFSMNPMPYLMEPSTSRPGEGATQGIVEEVLQALL	63		
QY	48	AAGDEFETRFRRTFSDLAAQLHVTGPSAQCRFTQVSDDELFGGGPNWGRLVAVFFVFCAALC	107		
		:    :    :    :    :    :    :    :    :			
Db	64	EATEEFELRYQRAFSDLTSQLHITQDTAQOSFQQVMGELFRDGTNWGR:VAFFSFGRALC	123		
QY	108	AESVNKEMEPLVGQVDKWVAYLETRLADWIHSSGGWAETALYGDGALEEARRLRE--G	165		
		:        :    :    :    :    :    :    :			
Db	124	VESANKEMTDLLPRIVQMVMNYJEHTLPQWYQENGGWAEFVCLYGKNAAQSRRESQBEPG	183		
QY	166	NWASVRTVLTTGAVAL	180		
		:    :			
Db	184	RLTLTI-VMLTGVFAL	197		

Search completed: October 24, 2003, 10:46:48  
Job time : 14.5 secs



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OM protein - protein search, using sw model

Run on: October 24, 2003, 10:43:10 ; Search time 62 Seconds  
(without alignments)  
803.293 Million cell updates/sec

Title: US-09-925-674A-9  
Perfect score: 1009  
Sequence: 1 MATPASTPTDTRALVADPVG.....LTGAVALGALVTVGAFASK 193

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archheap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1002	99.3	193	11	O88996	O88996 rattus norv
2	965	95.6	193	11	O8CGL4	O8CGL4 mus musculu
3	767	76.0	178	11	Q9CYW5	Q9CYW5 mus musculu
4	767	76.0	178	11	O8CFR2	O8CFR2 mus musculu
5	436.5	43.3	233	6	Q9MYW4	Q9MYW4 oryctoiaqus
6	432.5	42.9	233	11	O35844	O35844 mus musculu
7	429.5	42.6	233	6	Q8SQ42	Q8SQ42 felis silve
8	428.5	42.5	233	6	Q9N1A2	Q9N1A2 sus scrofa
9	425.5	42.2	233	6	Q9MZS7	Q9MZS7 ovis aries
10	409	40.5	236	11	Q8BQK4	Q8BQK4 mus musculu
11	401	39.7	180	6	Q9BD05	Q9BD05 bos taurus
12	401	39.7	217	11	Q99N35	Q99N35 mus musculu
13	399.5	39.6	180	6	Q9BDX7	Q9BDX7 bos taurus
14	397	39.3	238	13	Q90Z98	Q90Z98 brachydanio
15	395	39.1	236	11	Q923R6	Q923R6 cricetus
16	394.5	39.1	235	6	Q8I008	Q8I008 felis silve

17	371.5	36.8	188	11	Q9QWX2	Q9QWX2 mus musculu
18	371.5	36.8	235	11	O35843	O35843 mus musculu
19	369.5	36.6	188	4	Q9H1R6	Q9H1R6 homo sapien
20	368	36.5	204	13	Q90ZH2	Q90ZH2 xenopus lae
21	350	34.7	185	6	Q8MJ81	Q8MJ81 bos taurus
22	347	34.4	219	11	Q99N36	Q99N36 mus musculu
23	339.5	33.6	199	11	Q8C5P0	Q8C5P0 mus musculu
24	296	29.3	89	13	Q8UWJ1	Q8UWJ1 gallus gall
25	187	18.5	209	11	Q9JK59	Q9JK59 rattus norv
26	182	18.0	170	11	Q9WU15	Q9WU15 rattus norv
27	182	18.0	209	11	Q8C264	Q8C264 mus musculu
28	177.5	17.6	192	13	Q9I9N4	Q9I9N4 brachydanio
29	175.5	17.4	221	13	Q98U13	Q98U13 xenopus lae
30	173.5	17.2	190	4	Q8NFF3	Q8NFF3 homo sapien
31	165.5	16.4	125	4	Q9H1R5	Q9H1R5 homo sapien
32	163	16.2	235	5	Q967D2	Q967D2 geodia cydo
33	162	16.1	58	11	Q9R1B3	Q9R1B3 rattus norv
34	157.5	15.6	163	6	Q9MZS6	Q9MZS6 ovis aries
35	156.5	15.5	173	11	Q8K3J2	Q8K3J2 mus musculu
36	154	15.3	173	4	Q8WZ49	Q8WZ49 homo sapien
37	154	15.3	173	11	Q9JKL3	Q9JKL3 rattus norv
38	151	15.0	67	6	Q8MJB3	Q8MJB3 cervus elap
39	149	14.8	192	6	Q8SQ43	Q8SQ43 felis silve
40	148.5	14.7	218	5	Q9N754	Q9N754 suberites d
41	148	14.7	192	6	Q8HYU5	Q8HYU5 canis fami
42	147.5	14.6	179	4	Q9NYG7	Q9NYG7 homo sapien
43	145	14.4	149	6	Q9GMG7	Q9GMG7 ovis aries
44	144	14.3	177	13	Q90ZNI	Q90ZNI gallus gall
45	142	14.1	211	13	Q9W6F1	Q9W6F1 gallus gall

ALIGNMENTS

RESULT 1  
O88996  
ID O88996 PRELIMINARY; PRT; 193 AA.  
AC O88996;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Bcl-w.  
GN BCL-W.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
CX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain;  
RX MEDLINE=99292146; PubMed=10366024;  
RA Hamner S., Skoglosa Y., Lindholm D.;  
RT "Differential expression of bcl-w and bcl-x messenger RNA in the  
developing and adult rat nervous system.";  
RL Neuroscience 91:673-684(1999).  
DR EMBL; AF096291; AAC64200.1; -.  
DR HSSP; Q07817; IMAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS50063; BH4\_2; 1.  
SQ SEQUENCE 193 AA; 20820 MW; 36D6742F4529AFB4 CRC64;  
Query Match 99.3%; Score 1002; DB 11; Length 193;  
Best Local Similarity 99.0%; Pred. No. 1.2e-81;





DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)  
DE Bcl-xl protein.  
GN BCL-XL.  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Nagafuchi S., Sano J., Kano R., Hasegawa A.;  
RT "Molecular cloning of feline Bcl-2 family."  
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB080951; BAB85856.2; -  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS0063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26017 MW; CD17F24FE9D47BC9 CRC64;  
  
Query Match 42.6%; Score 429.5; DB 6; Length 233;  
Best Local Similarity 41.2%; Pred. No. 1.9e-30;  
Matches 96; Conservative 24; Mismatches 58; Indels 55; Gaps 5;  
  
QY 11 RALVADFGVYRLROKGY-----PLHQAMRAAGDEFETFRRTFSDLAALHVTGSAQORFT 80  
DQ 6 RELVDFLSYKLSQKGYSWRSFSDVEENRTEAPEGTESEMETPSAINGNPSWHLADSPAV 65  
  
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETFRRTFSDLAALHVTGSAQORFT 80  
DQ 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124  
  
QY 81 QVSDLEFQGGPNWRLVAVFFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHS 140  
DQ 125 QVWNELFRDGVNWGRIVAFFSFGALCVESVDKEMQVLVSRATWMTATYLNCHLEPWIQE 184  
  
QY 141 SGGWAEFTALYGDGALEEARLRN--GNWASVRTVLTGVALGALVTGVAFFASK 193  
DQ 185 NGGWDTFVELYGNNAEAESRK---GQERSNRWFLTGMTVAG-VLLGSLFSRK 233  
  
RESULT 8  
Q9N1A2 PRELIMINARY; PRT; 233 AA.  
AC Q9N1A2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anti-apoptotic regulator Bcl-XL.  
GN BCL-XL.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Lee T.L., Canty J.M.;  
RT "PCR Cloning of a Porcine bcl-xl cDNA from Heart."  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF216205; AAF3321.1; -  
DR HSSP; Q07817; 1MA2.

DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.  
DR PROSITE; PS0063; BH4\_2; 1.  
SQ SEQUENCE 233 AA; 26047 MW; 2FA312818B25E17D CRC64;  
  
Query Match 42.5%; Score 428.5; DB 6; Length 233;  
Best Local Similarity 41.3%; Pred. No. 2.3e-30;  
Matches 93; Conservative 22; Mismatches 57; Indels 53; Gaps 4;  
  
QY 11 RALVADFGVYRLROKGY-----PLHQAMRAAGDEFETFRRTFSDLAALHVTGSAQORFT 80  
DQ 6 RELVDFLSYKLSQKGYSWRSQFTDVEENRTEAPEGTESEATPSAINGNPSWHLADSPAV 65  
  
QY 29 CGAGPGEGPAAD-----PLHQAMRAAGDEFETFRRTFSDLAALHVTGSAQORFT 80  
DQ 66 NGA-TGHSSSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFE 124  
  
QY 81 QVSDLEFQGGPNWRLVAVFFVFGAALCAESVNKEMEPLVGQVQDMMVAYLETRLADWIHS 140  
DQ 125 QVWNELFRDGVNWGRIVAFFSFGALCVESVDKEMQVLVSRATWMTATYLNCHLEPWIQE 184  
  
QY 141 SGGWAEFTALYGDGALEEARLRN--GNWASVRTVLTGVALGAL 183  
DQ 185 NGGWDTFVELYGNNAEAESRKQERFNRWFLTGMTLAGVVLGSL 229  
  
RESULT 9  
Q9MZS7 PRELIMINARY; PRT; 233 AA.  
AC Q9MZS7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Bcl-x long protein.  
OS Ovis aries (Sheep).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Caprinae; Ovis.  
OX NCBI\_TaxID=9940;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Murray J.F., Dong Y.B., Leigh A.J., Scaramuzzi R.J., Carter N.D.;  
RT "Bcl-x in the sheep ovary."  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF164517; AAF89932.1; -  
DR HSSP; P53563; 1AF3.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; Bcl2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4; 1.



DR PROSITE; PS50063; BH4 2; 1.  
SQ SEQUENCE 233 AA; 26134 MW; 012BFA1382762915 CRC64;  
  
Query Match 42.2%; Score 425.5; DB 6; Length 233;  
Best Local Similarity 40.2%; Pred. No. 4.3e-30;  
Matches 90; Conservative 24; Mismatches 59; Indels 51; Gaps 4;  
  
QY 11 RALVADFVGYRLRQKV-----VCGAGP---GEGPAA 39  
DB 6 RELVDFLSYKLSQKGYSWQSFSDEENRTEAPEGTESDMETPSAINGNPSWHLADSPAV 65  
  
QY 40 D-----PLHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQ 81  
DB 66 NGATGHSRSLDAREVIPMAAVKQALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQ 125  
  
QY 82 VSDELFGQGNWGRVLVAFVFGAALCAESVNKEMEPLVGVQVQDMVAYLETRLADWIHSS 141  
DB 126 VVNELFRDGVNWGRIVAFPSFGGALCVESVDKEMQVLVSRIATWMTATYLNHLEPWIQEN 185  
  
QY 142 GGWAETALYGDGALAEARLRLE--GNWASVRVLTGAVALGAL 183  
DB 186 GGWDTFVELYGNNAAESRKGCERFNRWFLTGMTVAGVLLGSL 229  
  
RESULT 10  
Q8BQK4  
ID Q8BQK4 PRELIMINARY; PRT; 236 AA.  
AC Q8BQK4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE B-cell leukemia/lymphoma 2.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=body;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase 1 & 11 Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK049473; BAC33767.1; --  
SQ SEQUENCE 236 AA; 26437 MW; B726BFFA3AALC718 CRC64;  
  
Query Match 40.5%; Score 409; DB 11; Length 236;  
Best Local Similarity 37.1%; Pred. No. 1.3e-28;  
Matches 86; Conservative 35; Mismatches 59; Indels 52; Gaps 5;  
  
QY 9 DTRALVADFVGYRLRQKGYCGAG-----PG----- 34  
DB 10 ENREIVMKYIHYKLSQRGYEWDAAGDAAPLGAAPTFGIFSFQPESENPMVAHRDMAART 69  
  
QY 35 -----EGPAADP----LHQAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQ 81  
DB 70 SPLRPLVATTGPALSPVPPVHLTLRRAGDFFSRRYRDFAEISSQLHLTPFTARGRFAT 129  
  
QY 82 VSDELFGQGNWGRVLVAFVFGAALCAESVNKEMEPLVGVQVQDMVAYLETRLADWIHSS 141  
DB 130 VVEELFRDGVNWGRIVAFVFGVWCVESVNREMSPLVDNIALWMTETYNRHLHTWIQDN 189  
  
QY 142 GGWAETALYGDGALAEARLRLEGNWASVRTVLTGAVALGALVTVGAFFASK 193  
DB 190 GGWDAPVELYG----PSMRPLDFSWLSLKTLLSLAL-VGACITLGAYLGHK 236  
  
RESULT 11  
Q9BDD5  
ID Q9BDD5 PRELIMINARY; PRT; 180 AA.  
AC Q9BDD5;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE Anti-apoptotic regulator Bcl-xL (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Amills M., Bouzat J.;  
RT "Characterization of the bovine bcl-xL gene and related pseudogenes."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF245488; AAK31307.1; --  
DR EMBL; AF245489; AAK31308.1; --  
DR HSSP; Q07817; IMAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS50062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
FT NON\_TER 180  
SQ SEQUENCE 180 AA; 20062 MW; 95DC436F95DABDA6 CRC64;  
  
Query Match 39.7%; Score 401; DB 6; Length 180;  
Best Local Similarity 53.5%; Pred. No. 4.8e-28;  
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;  
  
QY 44 QAMRAAGDEFETFRRTFSDLAALQHLVTPGSAQQRFTQVSDLELFGQGNWGRVLVAFVFG 103  
DB 38 QALREAGDEFELRYRRAFSDLTSQLHITPGTAYQSFEQVNVNELFRDGVNWGRIVAFVFG 97  
  
QY 104 AALCAESVNKEMEPLVGVQVQDMVAYLETRLADWIHSSGGWAEFTALYGGGALAEARLR 163  
DB 98 GALCVESVDKEMQVLVSRIATWMTATYLNHLEPWIQENGWDTFVELYGNNAEAESRKQG 157  
  
QY 164 E--GNWASVRVLTGAVALGAL 183  
DB 158 ERFNRWFLTGMTVAGVLLGSL 179  
  
RESULT 12  
Q99N35  
ID Q99N35 PRELIMINARY; PRT; 217 AA.  
AC Q99N35;  
DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
DE B-cell leukemia/lymphoma x (Fragment).  
GN SCLX.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SvJ;  
RA Yang X.-F., Cantor H.;  
RT "Novel cDNA structure and genomic organization of apoptosis regulatory  
gene Bcl-x-gamma."  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF133282; AAK15455.1; --  
DR EMBL; AF133281; AAK15455.1; JOINED.  
DR HSSP; P53563; 1AF3.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.

DR SMART; SM00337; BCL; 1.  
DR TIGRFAMS; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
SQ SEQUENCE 217 AA; 24234 MW; 3BSA4E809A7DEF18 CRC64;  
  
Query Match 39.7%; Score 401; DB 11; Length 217;  
Best Local Similarity 53.5%; Pred. No. 6e-28;  
Matches 76; Conservative 19; Mismatches 45; Indels 2; Gaps 1;  
  
QY 44 QAMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQRFTQVSDELFGQGNWGRLVAFVFG 103  
Db 72 QALREAGDEFELRYRAFSDLTSQLHITPGTAYQSFQVNVNELFRDGVNWGRIVAFPSFG 131  
  
QY 104 AALCAESVNKEMEPVLGVQVQDMMVAYLETRLADWIHSSGGWAEFTALYGDGALEEARLR 163  
Db 132 GALCVESVDKEMQVLVSRIASWMATYLNDEHLEPWIQENGWDTFVDLYGNNAAESRKGQ 191  
  
QY 164 E-GNWASVRTVLTGAVALGAL 183  
Db 192 ERFNRWELTGMTVAGWVLLGSL 213  
  
RESULT 13  
Q9BDX7  
ID Q9BDX7 PRELIMINARY; PRT; 180 AA.  
AC Q9BDX7;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE Anti-apoptotic regulator Bcl-xL (Fragment).  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Amills M., Bouzat J.;  
RT "Characterization of the bovine bcl-xL gene and related pseudogenes."  
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF245487; AAK31306.1; -  
DR HSSP; Q07817; 1MAZ.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
FT NON\_TER 1  
FT NON\_TER 180  
SQ SEQUENCE 180 AA; 20056 MW; 62C4C0BD055SA9EF CRC64;  
  
Query Match 39.6%; Score 399.5; DB 6; Length 180;  
Best Local Similarity 47.1%; Pred. No. 6.5e-28;  
Matches 82; Conservative 23; Mismatches 58; Indels 11; Gaps 3;  
  
QY 20 YRLRQKGYVCGAGGEGPAAD-----PLHOAMRAAGDEFETRFRRTFSDLAALQHLVT 71  
Db 7 WHELDSPAUNGA-PGHSRSSDAREVIPMAAVKQALREAGDEFELRYRAFSDLTSQLHIT 65  
  
QY 72 PGSAQQRFTQVSDELFGQGNWGRLVAFVFGAALCAESVNKEMEPVLGVQVQDMMVAYLE 131  
Db 66 PGTAYQSFQVNVNELFRDGVNWGRIVASFSGGALCVESVDKEMQVLVSRITATWMTATYLN 125  
  
QY 132 TRLADWIHSSGGWAEFTALYGDGALEEARLRLE--GNWASVRTVLTGAVALGAL 183  
Db 126 DHLEPWIQENGWDTFVELYGNNAEAESRKGGRFNRWFLTGMTVAGWVLLGSL 179

RESULT 14  
Q9CZ98  
ID Q9CZ98 PRELIMINARY; PRT; 238 AA.  
AC Q9CZ98;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Bcl-XL-like protein 1.  
GN BCL2L OR BLP1.  
OS Brachydanio rerio (Zebrafish) (Danio rerio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
OC Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21299061; PubMed=11406282;  
RA Chen M.-C., Gong H.-Y., Cheng C., Wang J.-P., Hong J., Wu J.-L.;  
RT "Cloning and characterization of zfBLP1, a Bcl-XL homologue from the zebrafish, Danio rerio(1).";  
RL Biochim. Biophys. Acta 1519:127-133(2001).  
DR EMBL; AF317837; AAK81706.1; -  
DR ZFIN; ZDB-GENE-010730-1; bcl2l1.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR PROSITE; PS00062; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS00063; BH4\_2; 1.  
SQ SEQUENCE 238 AA; 26253 MW; 6E58394933EEFDDB CRC64;  
  
Query Match 39.3%; Score 397; DB 13; Length 238;  
Best Local Similarity 35.7%; Pred. No. 1.5e-27;  
Matches 85; Conservative 29; Mismatches 62; Indels 62; Gaps 6;  
  
QY 11 RALVADFGYRLRQKGYVC-----GAG----- 32  
Db 6 RELVVFFIKYKLSQRNYPCHGLTETDNRDTGAENGEGAAGATTLVNGTMNRTNASST 65  
  
QY 33 --PGECPAADPLHQ-----AMRAAGDEFETRFRRTFSDLAALQHLVTPGSAQQR 78  
Db 66 GTPPQSPASSPORQTNGSGGLDAVKEALRDSANEFELRYRAFNDLSSQLHITPATAYQS 125  
  
QY 79 FTQVSDELFGQGNWGRLVAFVFGAALCAESVNKEMEPVLGVQVQDMMVAYLETRLADWI 138  
Db 126 FESVMDVFRDGVNWGRIVGLFAFGGALCVCEKEMSPLVGRIAEWMTVYLDNHIQPMI 185  
  
QY 139 HSSGGWAEFTALYGDGALEEARLRREG--NWA-SVRTVLTGAVALGALVTVGAFFASK 193  
Db 186 QSQGGWERFAEIFGKDAAESRKSQESFKKWLFGMTLLTG-----VVVGGGLIAQK 236  
  
RESULT 15  
Q923R6  
ID Q923R6 PRELIMINARY; PRT; 236 AA.  
AC Q923R6;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE B-cell lymphoma protein 2.  
GN BCL2.  
OS Cricetulus longicaudatus (Long-tailed hamster) (Chinese hamster).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;  
OC Cricetulus.  
OX NCBI\_TaxID=10030;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Lai D.Z., Chen W., Wang H.T.;

RT "Construction of a robust CHO cell line for biopharmaceutical use.";  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF494339; AAK92201.1; -.  
DR InterPro; IPR000712; Bcl2\_BH.  
DR InterPro; IPR003093; Bcl2\_BH4.  
DR InterPro; IPR002475; BCL2\_family.  
DR InterPro; IPR004725; Bcl2\_reg.  
DR Pfam; PF00452; Bcl-2; 1.  
DR Pfam; PF02180; BH4; 1.  
DR SMART; SM00337; BCL; 1.  
DR SMART; SM00265; BH4; 1.  
DR TIGRFAMs; TIGR00865; bcl-2; 1.  
DR PROSITE; PS00662; BCL2\_FAMILY; 1.  
DR PROSITE; PS01080; BH1; 1.  
DR PROSITE; PS01258; BH2; 1.  
DR PROSITE; PS01259; BH3; 1.  
DR PROSITE; PS01260; BH4\_1; 1.  
DR PROSITE; PS00663; BH4\_2; 1.  
SQ SEQUENCE 236 AA; 26500 MW; BEDF052EF32CA8B8 CRC64;

Query Match		39.1%;	Score 395;	DB 11;	Length 236;
Best Local Similarity		34.9%;	Pred. No. 2.3e-27;		
Matches	81;	Conservative	33;	Mismatches	66;
			Indels	52;	Gaps
					3;
QY	9	DTRALVADFVGYRLRQGY	-----	27	
Db	10	DNREIVMKYIHYKLSQGYEWVGDVDAAPLGAAPTGGIFSEFQPESTPAVHRDMAART	69		
QY	28	-----VCGAGPGEGPAADPLHQAMRAAGDEFETPRRTFSDLAAQLHVTGSAQQRFTQ	81		
Db	70	SPLRPIVATTGPTLSPVPPVVEHJTLRRAGDDFSRRYRRDFAEMSSQLHLPFTARGREAT	129		
QY	82	VSDELFQGGFNWGRLVAFVFGAALCAESVNKEMEPLVGQVQDWMVAYLETRLADWIHSS	141		
Db	130	VVEELFRDGVNWGRIVAFPEFGVMCVESVNREMSPLVDNIALWMTVELNRHLHTWIQDN	189		
QY	142	GGWAEFTALYGDGGALEEARRLREGNWNASVRTVLTGAVALGALNTVGAFPAASK	193		
Db	190	GGWDAFVELYG---PSVRPLDFSWLSLXTLLNLAL-VGACITLGTYLGHK	236		

Search completed: October 24, 2003, 10:51:08  
Job time : 63 secs